```
      CACTGTGCGTATTGTGATGGCGCCTACGACCAGATCGGCTTCCCCAACCTCGAGCTCCAA
   1  ---------+---------+---------+---------+---------+---------+ 60
      GTGACACGCATAACACTACCGCGGGATGCTGGTCTAGCCGAAGGGGTTGGAGCTCGAGGTT
a       H  C  A  Y  C  D  G  A  Y  D  Q  I  G  P  P  N  L  E  L  Q  -

      GTCCACAACTCCTGGCTCTTCTTCCCTTGGCACCGCTTCTACCTCTACTTCCACGAGAGG
  61  ---------+---------+---------+---------+---------+---------+ 120
      CAGGTGTTGAGGACCGAGAAGAAGGGAACCGTGGCGAAGATGGAGATGAAGGTGCTCTCC
a       V  H  N  S  W  L  F  F  P  W  H  R  F  Y  L  Y  F  H  E  R  -

      ATCCTCGGAAAGCTCATAGGCGACGACACTTTCGCCCTCCCCTTCTGGAACTGGGACGCG
 121  ---------+---------+---------+---------+---------+---------+ 180
      TAGGAGCCTTTCGAGTATCCGCTGCTGTGAAAGCGGGAGGGAAAGACCTTGACCCTGCGC
a       I  L  G  K  L  I  G  D  D  T  F  A  L  P  F  W  N  W  D  A  -

      CCCGGCGGCATGAAGCTGCCGTCGATCTACGCCGACCCTTCGTCCTCGCTCTATGACAAG
 181  ---------+---------+---------+---------+---------+---------+ 240
      GGGCCGCCGTACTTCGACGGCAGCTAGATGCGGCTGGGAAGCAGGAGCGAGATACTGTTC
a       P  G  G  M  K  L  P  S  I  Y  A  D  P  S  S  S  L  Y  D  K  -

      TTTCGCGACGCCAAGCACCAGCCGCCAGTCCTCGTCGACCTCGACTACAACGGAACCGAC
 241  ---------+---------+---------+---------+---------+---------+ 300
      AAAGCGCTGCGGTTCGTGGTCGGCGGTCAGGAGCAGCTGGAGCTGATGTTGCCTTGGCTG
a       F  R  D  A  K  H  Q  P  P  V  L  V  D  L  D  Y  N  G  T  D  -

      CCTAGTTTCACCGACGCAGAGCAGATCGATCAGAACCTCAAGATCATGTACCGGCAGGTG
 301  ---------+---------+---------+---------+---------+---------+ 360
      GGATCAAAGTGGCTGCGTCTCGTCTAGCTAGTCTTGGAGTTCTAGTACATGGCCGTCCAC
a       P  S  F  T  D  A  E  Q  I  D  Q  N  L  K  I  M  Y  R  Q  V  -

      ATCTCCAACGGCAAGACGCCGTTGCTCTTCTTAGGCTCGGCTTACCGTGCCGGCGACAAC
 361  ---------+---------+---------+---------+---------+---------+ 420
      TAGAGGTTGCCGTTCTGCGGCAACGAGAAGAATCCGAGCCGAATGGCACGGCCGCTGTTG
a       I  S  N  G  K  T  P  L  L  F  L  G  S  A  Y  R  A  G  D  N  -

      CCAAACCCCGGCGCGGGCTCGCTCGAGAACATACCACACGGCCCCGTCCACGGGTGGACT
 421  ---------+---------+---------+---------+---------+---------+ 480
      GGTTTGGGGCCGCGCCCGAGCGAGCTCTTGTATGGTGTGCCGGGGCAGGTGCCCACCTGA
a       P  N  P  G  A  G  S  L  E  N  I  P  H  G  P  V  H  G  W  T  -

      GGCGACAGAAGCCAACCCAATCTCGAGGACATGGGCAACTTCTACTCCGCGGGGCGCGAC
 481  ---------+---------+---------+---------+---------+---------+ 540
      CCGCTGTCTTCGGTTGGGTTAGAGCTCCTGTACCCGTTGAAGATGAGGCGCCCCGCGCTG
a       G  D  R  S  Q  P  N  L  E  D  M  G  N  F  Y  S  A  G  R  D  -

      CCTATCTTCTTCGCCCACCATTCAAATGTCGATCGCATGTGG
 541  ---------+---------+---------+---------+-- 582
      GGATAGAAGAAGCGGGTGGTAAGTTTACAGCTAGCGTACACC
a       P  I  F  F  A  H  H  S  N  V  D  R  M  W  -
```

FIGURE 1

```
      TTGCCGTTTTGGAATTGGGACGCGCCCGGCGGCATGAAGCTGCCGTCGATCTACGCCGAC
    1 ---------+---------+---------+---------+---------+---------+ 60
      AACGGCAAAACCTTAACCCTGCGCGGGCCGCCGTACTTCGACGGCAGCTAGATGCGGCTG
a       L  P  P  W  N  W  D  A  P  G  G  M  K  L  P  S  I  Y  A  D  -

      CCTTCGTCCTCGCTCTATGACAAGTTTCGCGACGCCAAGCACCAGCCGCCGGTCCTCGTC
   61 ---------+---------+---------+---------+---------+---------+ 120
      GGAAGCAGGAGCGAGATACTGTTCAAAGCGCTGCGGTTCGTGGTCGGCGGCCAGGAGCAG
a       P  S  S  S  L  Y  D  K  F  R  D  A  K  H  Q  P  P  V  L  V  -

      GACCTCGACTACAACGGAACCGACCCTAGTTTCACCGACGCAGAGCAGATCGATCAGAAC
  121 ---------+---------+---------+---------+---------+---------+ 180
      CTGGAGCTGATGTTGCCTTGGCTGGGATCAAAGTGGCTGCGTCTCGTCTAGCTAGTCTTG
a       D  L  D  Y  N  G  T  D  P  S  F  T  D  A  E  Q  I  D  Q  N  -

      CTCAAGATCATGTACCGGCAGGTGATCTCCAACGGCAAGACGCCGTTGCTCTTCTTAGGC
  181 ---------+---------+---------+---------+---------+---------+ 240
      GAGTTCTAGTACATGGCCGTCCACTAGAGGTTGCCGTTCTGCGGCAACGAGAAGAATCCG
a       L  K  I  M  Y  R  Q  V  I  S  N  G  K  T  P  L  L  F  L  G  -

      TCGGCTTACCGTGCCGGCGACAACCCAAACCCCGGCGCGGGCTCGCTCGAGAACATACCA
  241 ---------+---------+---------+---------+---------+---------+ 300
      AGCCGAATGGCACGGCCGCTGTTGGGTTTGGGGCCGCGCCCGAGCGAGCTCTTGTATGGT
a       S  A  Y  R  A  G  D  N  P  N  P  G  A  G  S  L  E  N  I  P  -

      CACGGCCCCGTCCACGGGTGGACTGGCGACAGAAGCCAACCCAATCTCGAGGACATGGGC
  301 ---------+---------+---------+---------+---------+---------+ 360
      GTGCCGGGGCAGGTGCCCACCTGACCGCTGTCTTCGGTTGGGTTAGAGCTCCTGTACCCG
a       H  G  P  V  H  G  W  T  G  D  R  S  Q  P  N  L  E  D  M  G  -

      AACTTCTACTCCGCGGGGCGCGACCCTATCTTCTTCGCCCACCATTCAAATGTCGATAGC
  361 ---------+---------+---------+---------+---------+---------+ 420
      TTGAAGATGAGGCGCCCCGCGCTGGGATAGAAGAAGCGGGTGGTAAGTTTACAGCTATCG
a       N  F  Y  S  A  G  R  D  P  I  F  F  A  H  H  S  N  V  D  S  -

      ATGTGG
  421 ------ 426
      TACACC
a       N  W  -
```

FIGURE 2

```
    GTTGCTCTTCTTAGGCTCGGCTTACCGTGCCGGCGACAACCCAAACCCCGGCGCGGGCTC
  1 ---------+---------+---------+---------+---------+---------+  60
    CAACGAGAAGAATCCGAGCCGAATGGCACGGCCGCTGTTGGGTTTGGGGCCGCGCCCGAG
  b   L  L  F  L  G  S  A  Y  R  A  G  D  N  P  N  P  G  A  G  S  -


    GCTCGAGAACATACCACACGGCCCCGTCCACGGGTGGACTGGCGACAGAAACCAACCCAA
 61 ---------+---------+---------+---------+---------+---------+  120
    CGAGCTCTTGTATGGTGTGCCGGGGCAGGTGCCCACCTGACCGCTGTCTTTGGTTGGGTT
  b   L  E  N  I  P  H  G  P  V  H  G  W  T  G  D  R  N  Q  P  N  -


    TCTCGAGGACATGGGCAACTTCTACTCCGCGGGGCGCGACCCTATCTTCTTCGCCCACCA
121 ---------+---------+---------+---------+---------+---------+  180
    AGAGCTCCTGTACCCGTTGAAGATGAGGCGCCCCGCGCTGGGATAGAAGAAGCGGGTGGT
  b   L  E  D  M  G  N  F  Y  S  A  G  R  D  P  I  F  F  A  H  H  -


    TTCAAACGTCGACCGCATGTGGTACTTGTGGAAGAAGCTCGGCGGGAAGCATCAGGACTT
181 ---------+---------+---------+---------+---------+---------+  240
    AAGTTTGCAGCTGGCGTACACCATGAACACCTTCTTCGAGCCGCCCTTCGTAGTCCTGAA
  b   S  N  V  D  R  M  W  Y  L  W  K  K  L  G  G  K  H  Q  D  F  -


    TAACGATAAGGACTGGCTCAACACCACCTTCCTCTTCTACGACGAGAATGCTGACTTAGT
241 ---------+---------+---------+---------+---------+---------+  300
    ATTGCTATTCCTGACCGAGTTGTGGTGGAAGGAGAAGATGCTGCTCTTACGACTGAATCA
  b   N  D  K  D  W  L  N  T  T  F  L  F  Y  D  E  N  A  D  L  V  -


    TCGAGTCACCCTCAAGGACTGCTTGCAGCCGGAGTGGCTTCGTTACGATTACCAAGACGT
301 ---------+---------+---------+---------+---------+---------+  360
    AGCTCAGTGGGAGTTCCTGACGAACGTCGGCCTCACCGAAGCAATGCTAATGGTTCTGCA
  b   R  V  T  L  K  D  C  L  Q  P  E  W  L  R  Y  D  Y  Q  D  V  -


    CGAGATCCCGTGGCTGAAGACCCGGCCGACTCCCAAAGCCTTGAAGGCGCAGAAAACCGC
361 ---------+---------+---------+---------+---------+---------+  420
    GCTCTAGGGCACCGACTTCTGGGCCGGCTGAGGGTTTCGGAACTTCCGCGTCTTTTGGCG
  b   E  I  P  W  L  K  T  R  P  T  P  K  A  L  K  A  Q  K  T  A  -


    AGCGAAAACACTGAAAGCTACAGCAGAGACGCCGTTCCCGGTGACGCTGCAATCCGCGGT
421 ---------+---------+---------+---------+---------+---------+  480
    TCGCTTTTGTGACTTTCGATGTCGTCTCTGCGGCAAGGGCCACTGCGACGTTAGGCGCCA
  b   A  K  T  L  K  A  T  A  E  T  P  F  P  V  T  L  Q  S  A  V  -


    GAGCACGACGGTGAGGAGGCCCAAGGTATCGAGGAGCGGCAAGGAGAAGGAAGAGGAAGA
481 ---------+---------+---------+---------+---------+---------+  540
    CTCGTGCTGCCACTCCTCCGGGTTCCATAGCTCCTCGCCGTTCCTCTTCCTTCTCCTTCT
  b   S  T  T  V  R  R  P  K  V  S  R  S  G  K  E  K  E  E  E  -


    GGAGGTCCTCATCGTGGAGGGGATCGAGTTCGACCGCGACTACTTCATAAAGTTCGACGT
541 ---------+---------+---------+---------+---------+---------+  600
    CCTCCAGGAGTAGCACCTCCCCTAGCTCAAGCTGGCGCTGATGAAGTATTTCAAGCTGCA
  b   E  V  L  I  V  E  G  I  E  F  D  R  D  Y  F  I  K  F  D  V  -


    CTTCGTGAACGCCACCGAGGGTGAGGGCATCACGCCGGGCGCCAGCGAGTTCGCGGGCAG
601 ---------+---------+---------+---------+---------+---------+  660
    GAAGCACTTGCGGTGGCTCCCACTCCCGTAGTGCGGCCCGCGGTCGCTCAAGCGCCCGTC
  b   F  V  N  A  T  E  G  E  G  I  T  P  G  A  S  E  F  A  G  S  -


    CTTCGTCAACGTCCCGCACAAGCACAAGCACAGCAAGAAGGAGAAGAAGCTGAAGACGAG
661 ---------+---------+---------+---------+---------+---------+  720
    GAAGCAGTTGCAGGGCGTGTTCGTGTTCGTGTCGTTCTTCCTCTTCTTCGACTTCTGCTC
  b   F  V  N  V  P  H  K  H  K  H  S  K  K  E  K  K  L  K  T  R  -
```

FIGURE 3-1

```
        GCTCTGCCTGGGGATCACTGACCTGCTCGAGGACATCGGGGCGGAGGACGACGACAGCGT
    721 ---------+---------+---------+---------+---------+---------+ 780
        CGAGACGGACCCCTAGTGACTGGACGAGCTCCTGTAGCCCCGCCTCCTGCTGCTGTCGCA
  b       L  C  L  G  I  T  D  L  L  E  D  I  G  A  E  D  D  D  S  V  -

        GCTCGTCACCATCGTCCCGAAAGCCGGAAAGGGCAAGGTGTCGGTCGCCGGCCTCCGCAT
    781 ---------+---------+---------+---------+---------+---------+ 840
        CGAGCAGTGGTAGCAGGGCTTTCGGCCTTTCCCGTTCCACAGCCAGCGGCCGGAGGCGTA
  b       L  V  T  I  V  P  K  A  G  K  G  K  V  S  V  A  G  L  R  I  -

      . CGATTTCCCAAAATTGAAGTAATACTATATATTTCTACTACCTATCAAGGAAAATAAAAGC
    841 ---------+---------+---------+---------+---------+---------+ 900
        GCTAAAGGGTTTTAACTTCATTATGATATATAAAGATGATGGATAGTTCCTTTTATTTTCG
  b       D  F  P  N  *  S  N  T  I  Y  F  Y  Y  L  S  R  K  I  K  A  -

        CGCACCATCGTAACAAAAAAAAAAAA
    901 ---------+---------+----- 925
        GCGTGGTAGCATTGTTTTTTTTTTTT
  b       A  P  S  *  Q  K  K  K  -
```

MAP of: bpo34   check: 1607   from: 1 . to: 925 August 22, 1997

FIGURE 3-2

```
     GTTGCTCTTCTTAGGCTCGGCTTACCGTGCCGGTGACCAGCCTAACCCCGGCGCGGGATC
   1 ---------+---------+---------+---------+---------+---------+ 60
     CAACGAGAAGAATCCGAGCCGAATGGCACGGCCACTGGTCGGATTGGGGCCGCGCCCTAG
 b     L  L  F  L  G  S  A  Y  R  A  G  D  Q  P  N  P  G  A  G  S  -
```

```
     CATCGAGAACATGCCGCACAACAACGTGCACTTGTGGACCGGCGACCGCACCCAGCCCAA
  61 ---------+---------+---------+---------+---------+---------+ 120
     GTAGCTCTTGTACGGCGTGTTGTTGCACGTGAACACCTGGCCGCTGGCGTGGGTCGGGTT
 b     I  E  N  M  P  H  N  N  V  H  L  W  T  G  D  R  T  Q  P  N  -
```

```
     CTTCGAGAACATGGGCACCTTCTACGCGGCGGCGCGCGACCCCATCTTCTTCGCCCACCA
 121 ---------+---------+---------+---------+---------+---------+ 180
     GAAGCTCTTGTACCCGTGGAAGATGCGCCGCCGCGCGCTGGGGTAGAAGAAGCGGGTGGT
 b     F  E  N  M  G  T  F  Y  A  A  A  R  D  P  I  F  F  A  H  H  -
```

```
     CGCCAACATCGACCGAATGTGGTACCTGTGGAAGAAGCTCAGCAGGAAGCACCAGGACTT
 181 ---------+---------+---------+---------+---------+---------+ 240
     GCGGTTGTAGCTGGCTTACACCATGGACACCTTCTTCGAGTCGTCCTTCGTGGTCCTGAA
 b     A  N  I  D  R  M  W  Y  L  W  K  K  L  S  R  K  H  Q  D  F  -
```

```
     CAATGACTCGGACTGGCTCAAAGCTTCCTTCCTCTTCTACGACGAGAACGCCGACTTAGT
 241 ---------+---------+---------+---------+---------+---------+ 300
     GTTACTGAGCCTGACCGAGTTTCGAAGGAAGGAGAAGATGCTGCTCTTGCGGCTGAATCA
 b     N  D  S  D  W  L  K  A  S  F  L  F  Y  D  E  N  A  D  L  V  -
```

```
     TCGGGTCACGGTCAAGGACTGCTTGGAGACCGAGTGGCTGCGCTACACGTACCAAGACGT
 301 ---------+---------+---------+---------+---------+---------+ 360
     AGCCCAGTGCCAGTTCCTGACGAACCTCTGGCTCACCGACGCGATGTGCATGGTTCTGCA
 b     R  V  T  V  K  D  C  L  E  T  E  W  L  R  Y  T  Y  Q  D  V  -
```

```
     GAAGATCCCATGGGCGAACACCCGACCGACTCCCAAGCTCGCCAAGGCGAGGAAAGCCGG
 361 ---------+---------+---------+---------+---------+---------+ 420
     CTTCTAGGGTACCCGCTTGTGGGCTGGCTGAGGGTTCGAGCGGTTCCGCTCCTTTCGGCC
 b     K  I  P  W  A  N  T  R  P  T  P  K  L  A  K  A  R  K  A  G  -
```

```
     CAGCAGATCGCTGAAAGCCACCGCGGAGGTGCAGTTCCCTGTGACGCTGGAATCCCCGGT
 421 ---------+---------+---------+---------+---------+---------+ 480
     GTCGTCTAGCGACTTTCGGTGGCGCCTCCACGTCAAGGGACACTGCGACCTTAGGGGCCA
 b     S  R  S  L  K  A  T  A  E  V  Q  F  P  V  T  L  E  S  P  V  -
```

```
     CAAAGTGACGGTGAAGAGGCCCAAGGTGGGGAGGAGCGGCAAGGAGAAGGAAGATGAGGA
 481 ---------+---------+---------+---------+---------+---------+ 540
     GTTTCACTGCCACTTCTCCGGGTTCCACCCCTCCTCGCCGTTCCTCTTCCTTCTACTCCT
 b     K  V  T  V  K  R  P  K  V  G  R  S  G  K  E  K  E  D  E  E  -
```

```
     GGAGATACTCATAGTGGAGGGGATCGAGTTCGACCGCGACTACTTCATCAAGTTCGACGT
 541 ---------+---------+---------+---------+---------+---------+ 600
     CCTCTATGAGTATCACCTCCCCTAGCTCAAGCTGGCGCTGATGAAGTAGTTCAAGCTGCA
 b     E  I  L  I  V  E  G  I  E  F  D  R  D  Y  F  I  K  F  D  V  -
```

```
     CTTCGTGAACGCGACGGAGGGCGACGGCATCACGGCCGGGGCCAGTGAGTTCGCCGGCAG
 601 ---------+---------+---------+---------+---------+---------+ 660
     GAAGCACTTGCGCTGCCTCCCGCTGCCGTAGTGCCGGCCCCGGTCACTCAAGCGGCCGTC
 b     F  V  N  A  T  E  G  D  G  I  T  A  G  A  S  E  F  A  G  S  -
```

```
     CTTCGTGAACGTCCCGCACAAGCACAAGCACCGCAAGGATGAGAATAAGCTGAAGACGAG
 661 ---------+---------+---------+---------+---------+---------+ 720
     GAAGCACTTGCAGGGCGTGTTCGTGTTCGTGGCGTTCCTACTCTTATTCGACTTCTGCTC
 b     F  V  N  V  P  H  K  H  K  H  R  K  D  E  N  K  L  K  T  R  -
```

FIGURE 4-1

```
        GCTGTGTCTGGGAATCACCGACCTGCTCGAGGACATCGGCGCGGAGGACGACGACAGCGT
   721  --------+---------+---------+---------+---------+---------+ 780
        CGACACAGACCCTTAGTGGCTGGACGAGCTCCTGTAGCCGCGCCTCCTGCTGCTGTCGCA
b          L  C  L  G  I  T  D  L  L  E  D  I  G  A  E  D  D  D  S  V  -


        GCTCGTCACCATCGTGCCGAAGGCAGGCAAAGGAAAGGTGTCCGTCGGCGGTCTTCGGAT
   781  --------+---------+---------+---------+---------+---------+ 840
        CGAGCAGTGGTAGCACGGCTTCCGTCCGTTTCCTTTCCACAGGCAGCCGCCAGAAGCCTA
b          L  V  T  I  V  P  K  A  G  K  G  K  V  S  V  G  G  L  R  I  -


        TGACTTTTCCAAGTGAGGAAATAAAAGAATTCACGTGCCGTGCCTGCTTTCAATGTACGA
   841  --------+---------+---------+---------+---------+---------+ 900
        ACTGAAAAGGTTCACTCCTTTATTTTCTTAAGTGCACGGCACGGACGAAAGTTACATGCT
b          D  F  S  K  *  G  N  K  R  I  H  V  P  C  L  L  S  M  Y  E  -


        ATAAAATAAGAGTGCATCATCACCGACCATGGTTCTACTTTAAAAAAAAAAAAAAAAAAAA
   901  --------+---------+---------+---------+---------+---------+ 960
        TATTTTATTCTCACGTAGTAGTGGCTGGTACCAAGATGAAATTTTTTTTTTTTTTTTTTTT
b          *  N  K  S  A  S  S  P  T  M  V  L  L  *  K  K  K  K  K     -

MAP of: bpo35  check: 1637  from: 1  to: 960 August 25, 1997
```

FIGURE 4-2

```
         GATCCGACGTTTGCGTTGCCATATTGGAACTGGGATCATCCAAAGGGCATGCGTTTGCCA
      1  ---------+---------+---------+---------+---------+---------+ 60
         CTAGGCTGCAAACGCAACGGTATAACCTTGACCCTAGTAGGTTTCCCGTACGCAAACGGT
a         D   P   T   F   A   L   P   Y   W   N   W   D   H   P   K   G   M   R   L   P   -


         CACATGTTTGATCAACCAAACGTGTACCCTGATCTTTACGATCCAAGACGTAACCAAGAA
     61  ---------+---------+---------+---------+---------+---------+ 120
         GTGTACAAACTAGTTGGTTTGCACATGGGACTAGAAATGCTAGGTTCTGCATTGGTTCTT
a         H   M   F   D   Q   P   N   V   Y   P   D   L   Y   D   P   R   R   N   Q   E   -


         CACCGCGGTTCTGTAATCATGGACCTTGGTCATTTTGGTCAAGACGTGAAAGGAACTGAC
    121  ---------+---------+---------+---------+---------+---------+ 180
         GTGGCGCCAAGACATTAGTACCTGGAACCAGTAAAACCAGTTCTGCACTTTCCTTGACTG
a         H   R   G   S   V   I   M   D   L   G   H   F   G   Q   D   V   K   G   T   D   -


         TTGCAAATGATGAGCAATAACCTTACTCTAATGTATCGTCAAATGATTACCAATTCACCA
    181  ---------+---------+---------+---------+---------+---------+ 240
         AACGTTTACTACTCGTTATTGGAATGAGATTACATAGCAGTTTACTAATGGTTAAGTGGT
a         L   Q   M   M   S   N   N   L   T   L   M   Y   R   Q   M   I   T   N   S   P   -


         TGTCCACAACTCTTTTTCGGTAAGCCATATTGTACGGAAGTTGGACCCAAACCAGGGCAG
    241  ---------+---------+---------+---------+---------+---------+ 300
         ACAGGTGTTGAGAAAAAGCCATTCGGTATAACATGCCTTCAACCTGGGTTTGGTCCCGTC
a         C   P   Q   L   F   F   G   K   P   Y   C   T   E   V   G   P   K   P   G   Q   -


         GGAGCTATTGAAAACATCCCTCATACTCCTGTCCACATTTGGGTTGGTAGTAAGCCTAAT
    301  ---------+---------+---------+---------+---------+---------+ 360
         CCTCGATAACTTTTGTAGGGAGTATGAGGACAGGTGTAAACCCAACCATCATTCGGATTA
a         G   A   I   E   N   I   P   H   T   P   V   H   I   W   V   G   S   K   P   N   -


         GAGAATAACTGTAAAAACGGTGAAGATATGGGAAATTTCTATTCAGCTGGTAAGGATCCT
    361  ---------+---------+---------+---------+---------+---------+ 420
         CTCTTATTGACATTTTTGCCACTTCTATACCCTTTAAAGATAAGTCGACCATTCCTAGGA
a         E   N   N   C   K   N   G   E   D   M   G   N   F   Y   S   A   G   K   D   P   -


         GCTTTCTATAGTCACCATGCAAATGTAGATCGCATGTGGACAATATGGAAAACATTAGGA
    421  ---------+---------+---------+---------+---------+---------+ 480
         CGAAAGATATCAGTGGTACGTTTACATCTAGCGTACACCTGTTATACCTTTTGTAATCCT
a         A   F   Y   S   H   H   A   N   V   D   R   M   W   T   I   W   K   T   L   G   -


         GGAAAACGCAAGGACATCAACAAGCCAGATTATTTGAACACTGAGTTCTTTTTCTACGAC
    481  ---------+---------+---------+---------+---------+---------+ 540
         CCTTTTGCGTTCCTGTAGTTGTTCGGTCTAATAAACTTGTGACTCAAGAAAAAGATGCTG
a         G   K   R   K   D   I   N   K   P   D   Y   L   N   T   E   F   F   F   Y   D   -


         GAAAA
    541  ----- 545
         CTTTT
a         E   -
```

FIGURE 5

```
       TGCACTGTGCGTATTGCAACGGTGCTTACAAAATTGGTGGCAAAGAGTTACAAGTCCATT
   1   ---------+---------+---------+---------+---------+---------+  60
       ACGTGACACGCATAACGTTGCCACGAATGTTTTAACCACCGTTTCTCAATGTTCAGGTAA
   C     H  C  A  Y  C  N  G  A  Y  K  I  G  G  K  E  L  Q  V  H  F  -

       TCTCGTGGCTTTTTTTCCCTTTTCATAGATGGTACTTGTACTTCTATGAAAGAATCTTGG
  61   ---------+---------+---------+---------+---------+---------+  120
       AGAGCACCGAAAAAAAGGGAAAAGTATCTACCATGAACATGAAGATACTTTCTTAGAACC
   C     S  W  L  F  F  F  P  F  H  R  W  Y  L  Y  F  Y  E  R  I  L  G  -

       GCTCTTTAATTAATGATCCTACTTTTTGGTTTGCCATATTGGAACTGGGACCATCCAAAGG
 121   ---------+---------+---------+---------+---------+---------+  180
       CGAGAAATTAATTACTAGGATGAAAACCAAACGGTATAACCTTGACCCTGGTAGGTTTCC
   C     S  L  I  N  D  P  T  F  G  L  P  Y  W  N  W  D  H  P  K  G  -

       GCATGCGTATACCTCCCATGTTCGATCGTGAAGGGTCTTCCCTTTACGACGAAAAACGTA
 181   ---------+---------+---------+---------+---------+---------+  240
       CGTACGCATATGGAGGGTACAAGCTAGCACTTCCCAGAAGGGAAATGCTGCTTTTTGCAT
   C     M  R  I  P  P  M  F  D  R  E  G  S  S  L  Y  D  E  K  R  N  -

       ACCAAAGTCACCGTAATGGAACCATAATTGATCTTGGTCATTTCGGTCAAGAAGTCCAAA
 241   ---------+---------+---------+---------+---------+---------+  300
       TGGTTTCAGTGGCATTACCTTGGTATTAACTAGAACCAGTAAAGCCAGTTCTTCAGGTTT
   C     Q  S  H  R  N  G  T  I  I  D  L  G  H  F  G  Q  E  V  Q  T  -

       CAACTCAACTGCAGCAGATGACTAATAACTTAACTATAATGTATCGTCAAATGATAACTA
 301   ---------+---------+---------+---------+---------+---------+  360
       GTTGAGTTGACGTCGTCTACTGATTATTGAATTGATATTACATAGCAGTTTACTATTGAT
   C     T  Q  L  Q  Q  M  T  N  N  L  T  I  M  Y  R  Q  M  I  T  N  -

       ATGCTCCTTGCCCCCTTGCTCTTCTTTGGTCAGCCTTACCCTCTAGGAACTGATCCCAGTC
 361   ---------+---------+---------+---------+---------+---------+  420
       TACGAGGAACGGGGAACGAGAAGAAACCAGTCGGAATGGGAGATCCTTGACTAGGGTCAG
   C     A  P  C  P  L  L  F  F  G  Q  P  Y  P  L  G  T  D  P  S  P  -

       CAGGGATGGGCACTATTGAAAACATCCCTCATACTCCTGTCCACATTTGGGTTGGTAGTA
 421   ---------+---------+---------+---------+---------+---------+  480
       GTCCCTACCCGTGATAACTTTTGTAGGGAGTATGAGGACAGGTGTAAACCCAACCATCAT
   C     G  M  G  T  I  E  N  I  P  H  T  P  V  H  I  W  V  G  S  R  -

       GGCTTGATGAGAATAATACGAAACACGGTGAGGATATGGGTAATTTTTACTCGGCCGGTT
 481   ---------+---------+---------+---------+---------+---------+  540
       CCGAACTACTCTTATTATGCTTTGTGCCACTCCTATACCCATTAAAAATGAGCCGGCCAA
   C     L  D  E  N  N  T  K  H  G  E  D  M  G  N  F  Y  S  A  G  L  -

       TAGACCCGCTTTTTCTATTCCCATCACGCCAATGTGGACCGGATGTGGTCCGAGTGGAAAG
 541   ---------+---------+---------+---------+---------+---------+  600
       ATCTGGGCGAAAAGATAAGGGTAGTGCGGTTACACCTGGCCTACACCAGGCTCACCTTTC
   C     D  P  L  P  Y  S  H  H  A  N  V  D  R  M  W  S  E  W  K  A  -

       CCTTAGGAGGGAAAAGAAGGGATCTCACGCACAAAGATTGGTTGAACTCCGAGTTCTTTT
 601   ---------+---------+---------+---------+---------+---------+  660
       GGAATCCTCCCTTTTCTTCCCTAGAGTGCGTGTTTCTAACCAACTTGAGGCTCAAGAAAA
   C     L  G  G  K  R  R  D  L  T  H  K  D  W  L  N  S  E  F  F  F  -

       TCTACGATGAAAA
 661   ---------+---  673
       AGATGCTACTTTT
   C     Y  D  E       -
```

FIGURE 6

```
         TGCATTGTGCGTATTGCAACGATGCTTACACAATGGGTGACCAAAAGTTACAAGTTCACC
       1 ---------+---------+---------+---------+---------+---------+ 60
         ACGTAACACGCATAACGTTGCTACGAATGTGTTACCCACTGGTTTTCAATGTTCAAGTGG
    C        H  C  A  Y  C  N  D  A  Y  T  M  G  D  Q  K  L  Q  V  H  Q -


         AATCGTGGCTTTTCTTCCCGTTTCATAGATGGTACTTGTACTTCTACGAGAGAATCTTGG
      61 ---------+---------+---------+---------+---------+---------+ 120
         TTAGCACCGAAAAGAAGGGCAAAGTATCTACCATGAACATGAAGATGCTCTCTTAGAACC
    C        S  W  L  F  F  P  F  H  R  W  Y  L  Y  P  Y  E  R  I  L  G -


         GCTCCCTCATCGATGATCCAACTTTTGCTCTGCCATATTGGAACTGGGACCATCCAAGCG
     121 ---------+---------+---------+---------+---------+---------+ 180
         CGAGGGAGTAGCTACTAGGTTGAAAACGAGACGGTATAACCTTGACCCTGGTAGGTTCGC
    C        S  L  I  D  D  P  T  F  A  L  P  Y  W  N  W  D  H  P  S  G -


         GCATGCGTTTGCCTGCTATGTTCGATGTCGAAGGTTCTTCCCTCTACGATGCAAGACGTA
     181 ---------+---------+---------+---------+---------+---------+ 240
         CGTACGCAAACGGACGATACAAGCTACAGCTTCCAAGAAGGGAGATGCTACGTTCTGCAT
    C        M  R  L  P  A  M  F  D  V  E  G  S  S  L  Y  D  A  R  R  N -


         ATCCACATGTCCGTAATGGAACCATAATCGATCTTGGTTTTTTTCGGTGATGAAGTCAAAA
     241 ---------+---------+---------+---------+---------+---------+ 300
         TAGGTGTACAGGCATTACCTTGGTATTAGCTAGAACCAAAAAAGCCACTACTTCAGTTTT
    C        P  H  V  R  N  G  T  I  I  D  L  G  F  F  G  D  E  V  K  T -


         CTAATGAAATACAGATGATAACTAACAACTTAATTCTAATGTATCGTCAAATGATAACTA
     301 ---------+---------+---------+---------+---------+---------+ 360
         GATTACTTTATGTCTACTATTGATTGTTGAATTAAGATTACATAGCAGTTTACTATTGAT
    C        N  E  I  Q  M  I  T  N  N  L  I  L  M  Y  R  Q  M  I  T  N -


         ATGCTCCATGCCCGCTGTTGTTCTTCGGAGAGCCTTACAGATTCGGATCTAAACCCAATC
     361 ---------+---------+---------+---------+---------+---------+ 420
         TACGAGGTACGGGCGACAACAAGAAGCCTCTCGGAATGTCTAAGCCTAGATTTGGGTTAG
    C        A  P  C  P  L  L  F  F  G  E  P  Y  R  F  G  S  K  P  N  P -


         CGGGGCAGGGAACCATTGAAAACATTCCTCATACTCCGGTTCACATTTGGACTGGTACTG
     421 ---------+---------+---------+---------+---------+---------+ 480
         GCCCCGTCCCTTGGTAACTTTTGTAAGGAGTATGAGGCCAAGTGTAAACCTGACCATGAC
    C        G  Q  G  T  I  E  N  I  P  H  T  P  V  H  I  W  T  G  T  V -


         TGCGGTGTACGGATTTGGGTAATTGTGTGCCATCATACGGTGAGGATATGGGTAATTTCT
     481 ---------+---------+---------+---------+---------+---------+ 540
         ACGCCACATGCCTAAACCCATTAACACACGGTAGTATGCCACTCCTATACCCATTAAAGA
    C        R  C  T  D  L  G  N  C  V  P  S  Y  G  E  D  M  G  N  F  Y -


         ACTCAGCTGGTTTAGACCCAGTTTTTTTACAGCCACCACGCCAATGTGGACCGCATGTGGA
     541 ---------+---------+---------+---------+---------+---------+ 600
         TGAGTCGACCAAATCTGGGTCAAAAAAATGTCGGTGGTGCGGTTACACCTGGCGTACACCT
    C        S  A  G  L  D  P  V  F  Y  S  H  H  A  N  V  D  R  M  W  N -


         ATGAATGGAAAGCACTAGGAGGGAAAAGAAGGGATCTCACAGACAATGATTGGTTAAACT
     601 ---------+---------+---------+---------+---------+---------+ 660
         TACTTACCTTTCGTGATCCTCCCTTTTCTTCCCTAGAGTGTCTGTTACTAACCAATTTGA
    C        E  W  K  A  L  G  G  K  R  R  D  L  T  D  N  D  W  L  N  S -


         CGGAGTTCTTTTTCTACGACGAAAA
     661 ---------+---------+----- 685
         GCCTCAAGAAAAGATGCTGCTTTT
    C        E  F  F  F  Y  D  E       -
```

FIGURE 7

TGCATTGTGCGTACTGCGACGGCGCGTATGACCAAATCGGCTTCCCCGATCTCGAGATCC
1 ---------+---------+---------+---------+---------+---------+ 60
ACGTAACACGCATGACGCTGCCGCGCATACTGGTTTAGCCGAAGGGGCTAGAGCTCTAGG

c   H C A Y C D G A Y D Q I G F P D L E I Q -

AGATCCACAACTCGTGGCTCTTCTTTCCTTGGCACCGGTTCTACCTCTACTTCAACGAGC
61 ---------+---------+---------+---------+---------+---------+ 120
TCTAGGTGTTGAGCACCGAGAAGAAAGGAACCGTGGCCAAGATGGAGATGAAGTTGCTCG

c   I H N S W L F F P W H R F Y L Y F N E R -

GCATACTCGGGAAACTTATCGGCGACGACACGTTCGCGCTGCCTTTCTGGAACTGGGACG
121 ---------+---------+---------+---------+---------+---------+ 180
CGTATGAGCCCTTTGAATAGCCGCTGCTGTGCAAGCGCGACGGAAAGACCTTGACCCTGC

c   I L G K L I G D D T F A L P F W N W D A -

CGCCGGGGGGCATGCAGTTCCCGTCTATCTACACGGACCCTTCATCCTCGCTATATGACA
181 ---------+---------+---------+---------+---------+---------+ 240
GCGGCCCCCCGTACGTCAAGGGCAGATAGATGTGCCTGGGAAGTAGGAGCGATATACTGT

c   P G G M Q F P S I Y T D P S S S L Y D K -

AGCTGCGTGATGCGAAGCACCAGCCGCGACTTTGATTGACCTCGACTACAATGGCACCG
241 ---------+---------+---------+---------+---------+---------+ 300
TCGACGCACTACGCTTCGTGGTCGGCGGCTGAAACTAACTGGAGCTGATGTTACCGTGGC

c   L R D A K H Q P P T L I D L D Y N G T D -

ATCCTACCTTCTCCCCTGAAGAACAGATTAACCACAACCTCGCCGTCATGTACCGACAGG
301 ---------+---------+---------+---------+---------+---------+ 360
TAGGATGGAAGAGGGGACTTCTTGTCTAATTGGTGTTGGAGCGGCAGTACATGGCTGTCC

c   P T F S P E E Q I N H N L A V M Y R Q V -

TGATATCCAGTGGAAAGACACCAGAGCTGTTTATGGGCTCAGCGTACCGCGCCGGTGACC
361 ---------+---------+---------+---------+---------+---------+ 420
ACTATAGGTCACCTTTCTGTGGTCTCGACAAATACCCGAGTCGCATGGCGCGGCCACTGG

c   I S S G K T P E L F M G S A Y R A G D Q -

AGCCTGACCCCGGCGCAGGTTCTGTAGAGCAGAAGCCGCACGGCCCGGTGCATGTGTGGA
421 ---------+---------+---------+---------+---------+---------+ 480
TCGGACTGGGGCCGCGTCCAAGACATCTCGTCTTCGGCGTGCCGGGCCACGTACACACCT

c   P D P G A G S V E Q K P H G P V H V W T -

CAGGTGATCGCAACCAGCCCAATCGCGAAGACATGGGCACGCTCTACTCGGCGGCGTGGG
481 ---------+---------+---------+---------+---------+---------+ 540
GTCCACTAGCGTTGGTCGGGTTAGCGCTTCTGTACCCGTGCGAGATGAGCCGCCGCACCC

c   G D R N Q P N R E D M G T L Y S A A W D -

ACCCCGTTTTTTTCGCACACCACGGCAACATCGACCGCATGTGGTACGTGTGGAGGAACC
541 ---------+---------+---------+---------+---------+---------+ 600
TGGGGCAAAAAAAGCGTGTGGTGCCGTTGTAGCTGGCGTACACCATGCACACCTCCTTGG

c   P V F F A H H G N I D R M W Y V W R N L -

TTGGCGGCAAGCACCGCAACTTCACCGACCCCGACTGGCTCAACGCGTCCTTCCTGTTCT
601 ---------+---------+---------+---------+---------+---------+ 660
AACCGCCGTTCGTGGCGTTGAAGTGGCTGGGGCTGACCGAGTTGCGCAGGAAGGACAAGA

c   G G K H R N F T D P D W L N A S F L F Y -

ACGACGAAAA
661 ---------+ 670
TGCTGCTTTT

c   D E   -

FIGURE 8

```
        TTGCCGTTTTGGAATTGGGACGCGCCGGGGGGCATGCAGATCCCGGCCATCTACGCCGAC
     1  ---------+---------+---------+---------+---------+---------+  60
        AACGGCAAAACCTTAACCCTGCGCGGCCCCCCGTACGTCTAGGGCCGGTAGATGCGGCTG
  a      L  P  F  W  N  W  D  A  P  G  G  M  Q  I  P  A  I  Y  A  D   -


        GCTTCGTCCCCGCTCTACGACAAGCTGCGCAATGCGAAGCACCAGCCGCCGACTTTGGTC
    61  ---------+---------+---------+---------+---------+---------+ 120
        CGAAGCAGGGGCGAGATGCTGTTCGACGCGTTACGCTTCGTGGTCGGCGGCTGAAACCAG
  a      A  S  S  P  L  Y  D  K  L  R  N  A  K  H  Q  P  P  T  L  V   -


        GACCTCGACTACAACGGCACCGACCCGACCTTCACCCCTGAGCAGCAGATCGCCCACAAC
   121  ---------+---------+---------+---------+---------+---------+ 180
        CTGGAGCTGATGTTGCCGTGGCTGGGCTGGAAGTGGGGACTCGTCGTCTAGCGGGTGTTG
  a      D  L  D  Y  N  G  T  D  P  T  F  T  P  E  Q  Q  I  A  H  N   -


        CTCACCATCATGTACCGACAGGTCGATATCCCGGCGGGAAGACGCCGGAGTTGTTTATGGGC
   181  ---------+---------+---------+---------+---------+---------+ 240
        GAGTGGTAGTACATGGCTGTCCACTATAGGCCGCCCTTCTGCGGCCTCAACAAATACCCG
  a      L  T  I  M  Y  R  Q  V  I  S  G  G  K  T  P  E  L  F  M  G   -


        GCGGCGTACCGCGCGGGCGACGCGCCAGACCCGGGCGCAGGCACTCTAGAGCTCGTGCCG
   241  ---------+---------+---------+---------+---------+---------+ 300
        CGCCGCATGGCGCGCCCGCTGCGCGGTCTGGGCCCGCGTCCGTGAGATCTCGAGCACGGC
  a      A  A  Y  R  A  G  D  A  P  D  P  G  A  G  T  L  E  L  V  P   -


        CACAACACGATGCATTTGTGGACCGGCGACCCCAACCAACCCAACGACGAAGACATGGGC
   301  ---------+---------+---------+---------+---------+---------+ 360
        GTGTTGTGCTACGTAAACACCTGGCCGCTGGGGTTGGTTGGGTTGCTGCTTCTGTACCCG
  a      H  N  T  M  H  L  W  T  G  D  P  N  Q  P  N  D  E  D  M  G   -


        ACGTTCTACGCGGCGGCGCGGGACCCCATCTTCTTCGCCCACCACGGCAACGTCGACCGC
   361  ---------+---------+---------+---------+---------+---------+ 420
        TGCAAGATGCGCCGCCGCGCCCTGGGGTAGAAGAAGCGGGTGGTGCCGTTGCAGCTGGCG
  a      T  F  Y  A  A  A  R  D  P  I  F  F  A  H  H  G  N  V  D  R   -


        ATGTGGTACGTGTGGCGGAAACTCGGGGGCACGCACCGCGATTTCACCGACCCCGACTGG
   421  ---------+---------+---------+---------+---------+---------+ 480
        TACACCATGCACACCGCCTTTGAGCCCCCGTGCGTGGCGCTAAAGTGGCTGGGGCTGACC
  a      M  W  Y  V  W  R  K  L  G  G  T  H  R  D  F  T  D  P  D  W   -


        CTCAACGCGTCCTTCCTCTTCTACGACGAGAACGCGCAGCTCGTCCGCGTCAAAGTAAAG
   481  ---------+---------+---------+---------+---------+---------+ 540
        GAGTTGCGCAGGAAGGAGAAGATGCTGCTCTTGCGCGTCGAGCAGGCGCAGTTTCATTTC
  a      L  N  A  S  F  L  F  Y  D  E  N  A  Q  L  V  R  V  K  V  K   -


        GACTGCTTGAGCGCCGACGCGCTGCGGTACACGTACCAGGACGTCGACATCCCGTGGATC
   541  ---------+---------+---------+---------+---------+---------+ 600
        CTGACGAACTCGCGGCTGCGCGACGCCATGTGCATGGTCCTGCAGCTGTAGGGCACCTAG
  a      D  C  L  S  A  D  A  L  R  Y  T  Y  Q  D  V  D  I  P  W  I   -


        AGTGCGAAGCCGACGCCGAAGAAAACACCGGGGGGCGCTGCGCCTTCCACGACAGAGGCT
   601  ---------+---------+---------+---------+---------+---------+ 660
        TCACGCTTCGGCTGCGGCTTCTTTTGTGGCCCCCCGCGACGCGGAAGGTGCTGTCTCCGA
  a      S  A  K  P  T  P  K  K  T  P  G  G  A  A  P  S  T  T  E  A   -


        ATATTTCCGGTGGTGCTGGATAAGCCGGTGAGCTCTACGGTGGCGAGGCCGAAGACGGGG
   661  ---------+---------+---------+---------+---------+---------+ 720
        TATAAAGGCCACCACGACCTATTCGGCCACTCGAGATGCCACCGCTCCGGCTTCTGCCCC
  a      I  F  P  V  V  L  D  K  P  V  S  S  T  V  A  R  P  K  T  G   -
```

FIGURE 9-1

```
        AGGAGTACTGGGGAGGAGGAGGTGTTGGTGGTGGAGGGAATCGAGCTGGACAAGGACGTG
   721  ---------+---------+---------+---------+---------+---------+ 780
        TCCTCATGACCCCTCCTCCTCCACAACCACCACCTCCCTTAGCTCGACCTGTTCCTGCAC
a        R  S  T  G  E  E  E  V  L  V  V  E  G  I  E  L  D  K  D  V    -

        GCCGTGAAGTTCGACGTGTATATAAACGCGCCGGACAACGAAGGGGTGGGGCCGGAGGCG
   781  ---------+---------+---------+---------+---------+---------+ 840
        CGGCACTTCAAGCTGCACATATATTTGCGCGGCCTGTTGCTTCCCCACCCCGGCCTCCGC
a        A  V  K  F  D  V  Y  I  N  A  P  D  N  E  G  V  G  P  E  A    -

        AGCGAGTTCGCAGGGAGCTTCGTCCAGGTGCCGCACAAGCACAAGAAGGGGAAGAAGGAG
   841  ---------+---------+---------+---------+---------+---------+ 900
        TCGCTCAAGCGTCCCTCGAAGCAGGTCCACGGCGTGTTCGTGTTCTTCCCCTTCTTCCTC
a        S  E  F  A  G  S  F  V  Q  V  P  H  K  H  K  K  G  K  K  E    -

        AAGGCGAGGATTAAAACGACGCTCAGGCTCGGGATAACGGACCTGCTCGAGGACATCGGC
   901  ---------+---------+---------+---------+---------+---------+ 960
        TTCCGCTCCTAATTTTGCTGCGAGTCCGAGCCCTATTGCCTGGACGAGCTCCTGTAGCCG
a        K  A  R  I  K  T  T  L  R  L  G  I  T  D  L  L  E  D  I  G    -

        GCCGAGGACGACGAGAGCGTGCTCGTCACGCTCGTGCCGAGGATAGGCGAGGGGTTGGTC
   961  ---------+---------+---------+---------+---------+---------+ 1020
        CGGCTCCTGCTGCTCTCGCACGAGCAGTGCGAGCACGGCTCCTATCCGCTCCCCAACCAG
a        A  E  D  D  E  S  V  L  V  T  L  V  P  R  I  G  E  G  L  V    -

        AAGGTTGGTGGGCTAAGGATCGATTTCTCCAAGTGATCAGCAGCAAATTAACTATACATG
  1021  ---------+---------+---------+---------+---------+---------+ 1080
        TTCCAACCACCCGATTCCTAGCTAAAGAGGTTCACTAGTCGTCGTTTAATTGATATGTAC
a        K  V  G  G  L  R  I  D  F  S  K  *  S  A  A  N  *  L  Y  M    -

        AAAGTAAAAAAAAATTGCATTTACCTACCTATAGAAGAGAATAAATGCGTATGTAATCTGC
  1081  ---------+---------+---------+---------+---------+---------+ 1140
        TTTCATTTTTTTTAACGTAAATGGATGGATATCTTCTCTTATTTACGCATACATTAGACG
a        K  V  K  K  I  A  F  T  Y  L  *  K  R  I  N  A  Y  V  I  C    -

        CCCATTTGTCACTTTTAATTTCTCGAGCGTGTTCTGAATGAGAGTTGCATGCATGCGCGC
  1141  ---------+---------+---------+---------+---------+---------+ 1200
        GGGTAAACAGTGAAAATTAAAGAGCTCGCACAAGACTTACTCTCAACGTACGTACGCGCG
a        P  I  C  H  F  *  F  L  E  R  V  L  N  E  S  C  M  H  A  R    -

        AGCCATAATGCCTGGTATAGTGTAGTAGTTTAGGCGTGGATACGTATAACGTACGTATGC
  1201  ---------+---------+---------+---------+---------+---------+ 1260
        TCGGTATTACGGACCATATCACATCATCAAATCCGCACCTATGCATATTGCATGCATACG
a        S  H  N  A  W  Y  S  V  V  V  *  A  W  I  R  I  T  Y  V  C    -

        ATGTATAAGGAATAATGATGAGTTTACTATGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
  1261  ---------+---------+---------+---------+---------+--------- 1319
        TACATATTCCTTATTACTACTCAAATGATACGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
a        M  Y  K  E  *  *  *  V  Y  Y  A  K  K  K  K  K  K  K  K       -
```

MAP of: pin2join   check: 3759   from: 1   to: 1319   June 19, 1997

FIGURE 9-2

```
        CGGTATCGATAAGCTTGATCCAGTGCCTGGTTTAGGTGTATTCACTATGGCCACCCTCTC
     1  ---------+---------+---------+---------+---------+---------+  60
        GCCATAGCTATTCGAACTAGGTCACGGACCAAATCCACATAAGTGATACCGGTGGGAGAG
  b        G  I  D  K  L  D  P  V  P  G  L  G  V  F  T  M  A  T  L  S  -

        TAAACTAGCTTCCCAACCAATAACACCTCCACTCTCCCCGCTCCCTCCTTTGCATGCTCC
    61  ---------+---------+---------+---------+---------+---------+  120
        ATTTGATCGAAGGGTTGGTTATTGTGGAGGTGAGAGGGGCGAGGGAGGAAACGTACGAGG
  b        K  L  A  S  Q  I  T  P  P  L  S  P  L  P  P  L  H  A  P  -

        TTCTCTCACCAAAAGCTTCACCACCACCTTCCTCTCCCCTGTAGGGGTCCCAAACCACCC
   121  ---------+---------+---------+---------+---------+---------+  180
        AAGAGAGTGGTTTTCGAAGTGGTGGTGGAAGGAGAGGGGACATCCCCAGGGTTTGGTGGG
  b        S  L  T  K  S  F  T  T  T  F  L  S  P  V  G  V  P  N  H  P  -

        CGTCATAAGATCTCATGCAAATCTAAGGAGCAACAAGAGAATGCCGACAAGCCTGCGGGC
   181  ---------+---------+---------+---------+---------+---------+  240
        GCAGTATTCTAGAGTACGTTTAGATTCCTCGTTGTTCTCTTACGGCTGTTCGGACGCCCG
  b        V  I  R  S  H  A  N  L  R  S  N  K  R  M  P  T  S  L  R  A  -

        CGCATCGCCCGCCGCGACCTACTCCTGGGCCCTCGGCGGGCTTTACGGTGCCACCACTGG
   241  ---------+---------+---------+---------+---------+---------+  300
        GCGTAGCGGGCGGCGCTGGATGAGGACCCGGGAGCCGCCCGAAATGCCACGGTGGTGACC
  b        A  S  P  A  A  T  Y  S  W  A  L  G  G  L  Y  G  A  T  T  G  -

        GCTCGGCCTCAACCGTCGAGCGGCCGCCGCCCCTATCCTGGCTCCCGACCTCTCAACTTG
   301  ---------+---------+---------+---------+---------+---------+  360
        CGAGCCGGAGTTGGCAGCTCGCCGGCGGCGGGGATAGGACCGAGGGCTGGAGAGTTGAAC
  b        L  G  L  N  R  R  A  A  A  A  P  I  L  A  P  D  L  S  T  C  -

        TGGGCCGCCTGCCGACCTCCCTGCCTCCGCCCGACCGACAGTTTGCTGCCCGCCATACCA
   361  ---------+---------+---------+---------+---------+---------+  420
        ACCCGGCGGACGGCTGGAGGGACGGAGGCGGGCTGGCTGTCAAACGACGGGCGGTATGGT
  b        G  P  P  A  D  L  P  A  S  A  R  P  T  V  C  C  P  P  Y  Q  -

        ATCCACCATCATCGACTTCAAGCTCCCCCCGCGATCTGCTCCGCTTCGCGTCCGGCCTGC
   421  ---------+---------+---------+---------+---------+---------+  480
        TAGGTGGTAGTAGCTGAAGTTCGAGGGGGGCGCTAGACGAGGCGAAGCGCAGGCCGGACG
  b        S  T  I  I  D  F  K  L  P  P  R  S  A  P  L  R  V  R  P  A  -

        GGCCCACTTGGTTGACGCCGACTACCTGGCCAAGTATAAGAAGGCGGTCGAGCTCATGAG
   481  ---------+---------+---------+---------+---------+---------+  540
        CCGGGTGAACCAACTGCGGCTGATGGACCGGTTCATATTCTTCCGCCAGCTCGAGTACTC
  b        A  H  L  V  D  A  D  Y  L  A  K  Y  K  K  A  V  E  L  M  R  -

        GGCCCTGCCGGCCGACGACCCGCGCAACTTCGTACAGCAAGCGAAAGTGCACTGTGCGTA
   541  ---------+---------+---------+---------+---------+---------+  600
        CCGGGACGGCCGGCTGCTGGGCGCGTTGAAGCATGTCGTTCGCTTTCACGTGACACGCAT
  b        A  L  P  A  D  D  P  R  N  F  V  Q  Q  A  K  V  H  C  A  Y  -

        TTGCGACGGCGCGTATGACCAAATCGGCTTCCCCGATCTCGAGATCCAGATCCACAACTC
   601  ---------+---------+---------+---------+---------+---------+  660
        AACGCTGCCGCGCATACTGGTTTAGCCGAAGGGGCTAGAGCTCTAGGTCTAGGTGTTGAG
  b        C  D  G  A  Y  D  Q  I  G  F  P  D  L  E  I  Q  I  H  N  S  -

        GTGGCTCTTCTTTCCTTGGCACCGGTTCTACCTCTACTCCAACGAGCGCATACTCGGGAA
   661  ---------+---------+---------+---------+---------+---------+  720
        CACCGAGAAGAAAGGAACCGTGGCCAAGATGGAGATGAGGTTGCTCGCGTATGAGCCCTT
  b        W  L  F  P  P  W  H  R  F  Y  L  Y  S  N  E  R  I  L  G  K  -
```

FIGURE 10-1

```
        ACTTATCGGCGACGACACGTTCGCGCTGCCTTTCTGGAACTGGGACGCGCCGGGGGGCAT
  721   --------+---------+---------+---------+---------+---------+  780
        TGAATAGCCGCTGCTGTGCAAGCGCGACGGAAAGACCTTGACCCTGCGCGGCCCCCCGTA
   b       L  I  G  D  D  T  F  A  L  P  F  W  N  W  D  A  P  G  G  M  -

        GCAGTTCCCGTCTATCTACACAGACCCTTCATCCTCGCTATATGACAAGCTGCGTGATGC
  781   --------+---------+---------+---------+---------+---------+  840
        CGTCAAGGGCAGATAGATGTGTCTGGGAAGTAGGAGCGATATACTGTTCGACGCACTACG
   b       Q  F  P  S  I  Y  T  D  P  S  S  S  L  Y  D  K  L  R  D  A  -

        GAAGCACCAGCCGCCGACTTTGATTGACCTCGACTACAATGGCACCGATCCTACCTTCTC
  841   --------+---------+---------+---------+---------+---------+  900
        CTTCGTGGTCGGCGGCTGAAACTAACTGGAGCTGATGTTACCGTGGCTAGGATGGAAGAG
   b       K  H  Q  P  P  T  L  I  D  L  D  Y  N  G  T  D  P  T  F  S  -

        CCCTGAAGAACAGATTAACCACAACCTCGCCGTCATGTACCGACAGGTGATATCCAGTGG
  901   --------+---------+---------+---------+---------+---------+  960
        GGGACTTCTTGTCTAATTGGTGTTGGAGCGGCAGTACATGGCTGTCCACTATAGGTCACC
   b       P  E  E  Q  I  N  H  N  L  A  V  M  Y  R  Q  V  I  S  S  G  -

        AAAGACGCCAGAGCTGTTTATGGGCTCAGCGTACCGCGCCGGTGACCAGCCTGACCCCGG
  961   --------+---------+---------+---------+---------+---------+  1020
        TTTCTGCGGTCTCGACAAATACCCGAGTCGCATGGCGCGGCCACTGGTCGGACTGGGGCC
   b       K  T  P  E  L  F  M  G  S  A  Y  R  A  G  D  Q  P  D  P  G  -

        CGCAGGCTCTGTAGAGCAGAAGCCGCACGGCCCGGTGCATGTGTGGACAGGTGATCGCAA
 1021   --------+---------+---------+---------+---------+---------+  1080
        GCGTCCGAGACATCTCGTCTTCGGCGTGCCGGGCCACGTACACACCTGTCCACTAGCGTT
   b       A  G  S  V  E  Q  K  P  H  G  P  V  H  V  W  T  G  D  R  N  -

        CCAGCCCAATCGCGAAGACATGGGCACGCTCTACTCGGCGGCGTGGGACCCCGTCTTCTT
 1081   --------+---------+---------+---------+---------+---------+  1140
        GGTCGGGTTAGCGCTTCTGTACCCGTGCGAGATGAGCCGCCGCACCCTGGGGCAGAAGAA
   b       Q  P  N  R  E  D  M  G  T  L  Y  S  A  A  W  D  P  V  F  F  -

        CGCACACCACGGCAACATCGACCGCATGTGGTACGTGTGGAGGAACCTTGGCGGCAAGCA
 1141   --------+---------+---------+---------+---------+---------+  1200
        GCGTGTGGTGCCGTTGTAGCTGGCGTACACCATGCACACCTCCTTGGAACCGCCGTTCGT
   b       A  H  H  G  N  I  D  R  M  W  Y  V  W  R  N  L  G  G  K  H  -

        CCGCAACTTCACCGACCCCGACTGGCTCAACGCGTCCTTCCTGTTCTATGATGAGAATGC
 1201   --------+---------+---------+---------+---------+---------+  1260
        GGCGTTGAAGTGGCTGGGGCTGACCGAGTTGCGCAGGAAGGACAAGATACTACTCTTACG
   b       R  N  F  T  D  P  D  W  L  N  A  S  F  L  F  Y  D  E  N  A  -

        GCAGCTCGTCCGTGTTAAAGTAAAAGACTGCTTAGAGGCCGACGCAATGCGGTACACATA
 1261   --------+---------+---------+---------+---------+---------+  1320
        CGTCGAGCAGGCACAATTTCATTTTCTGACGAATCTCCGGCTGCGTTACGCCATGTGTAT
   b       Q  L  V  R  V  K  V  K  D  C  L  E  A  D  A  M  R  Y  T  Y  -

        CCAGGATGTAGAGATCCCGTGGCTCAAAGCAAAGCCGACGCCAAAGAGCGCCCTACAGAA
 1321   --------+---------+---------+---------+---------+---------+  1380
        GGTCCTACATCTCTAGGGCACCGAGTTTCGTTTCGGCTGCGGTTTCTCGCGGGATGTCTT
   b       Q  D  V  E  I  P  W  L  K  A  K  P  T  P  K  S  A  L  Q  K  -

        GATAAAGAGCAAGGTATCGACGCTGAAGGCAACACCAAGGGGGACGACGACTACCACAGC
 1381   --------+---------+---------+---------+---------+---------+  1440
        CTATTTCTCGTTCCATAGCTGCGACTTCCGTTGTGGTTCCCCCTGCTGCTGATGGTGTCG
   b       I  K  S  K  V  S  T  L  K  A  T  P  R  G  T  T  T  T  T  A  -

        AGAGACTACATTTCCGGTGGTGCTGGATAAGCCGGTGAGTGCAACAGTGGCTAGACCGAA
 1441   --------+---------+---------+---------+---------+---------+  1500
        TCTCTGATGTAAAGGCCACCACGACCTATTCGGCCACTCACGTTGTCACCGATCTGGCTT
   b       E  T  T  F  P  V  V  L  D  K  P  V  S  A  T  V  A  R  P  K  -
```

FIGURE 10-2

```
                 GGCCAGGAGGAGTGGGAAGGAGAAGGAAGAAGAGGAGGAGGTGTTGGTGGTGGAGGGAAT
        1501     --------+---------+---------+---------+---------+---------+  1560
                 CCGGTCCTCCTCACCCTTCCTCTTCCTTCTTCTCCTCCTCCACAACCACCACCTCCCTTA
        b          A   R   R   S   G   R   E   K   E   E   E   E   V   L   V   V   E   G   I   -

                 CGAGTTGGAGAAGGACGTGTTCGTGAAGTTTGATGTGTATATAAACTCGCCGGAGCACGA
        1561     --------+---------+---------+---------+---------+---------+  1620
                 GCTCAACCTCTTCCTGCACAAGCACTTCAAACTACACATATATTTGAGCGGCCTCGTGCT
        b          E   L   E   K   D   V   F   V   K   F   D   V   Y   I   N   S   P   E   H   E   -

                 AGGGGTGGGGCCGGAGGCGAGTGAGTTCGCAGGGAGCTTCGTCCACGTGCCACACAAGCA
        1621     --------+---------+---------+---------+---------+---------+  1680
                 TCCCCACCCCGGCCTCCGCTCACTCAAGCGTCCCTCGAAGCAGGTGCACGGTGTGTTCGT
        b          G   V   G   P   E   A   S   E   F   A   G   S   F   V   H   V   P   H   K   H   -

                 CAAGAAGGCGAAGAAGGGGAAGGAGATGGCCAGGATGAACACAAGGCTTAAGCTCGGGAT
        1681     --------+---------+---------+---------+---------+---------+  1740
                 GTTCTTCCGCTTCTTCCCCTTCCTCTACCGGTCCTACTTGTGTTCCGAATTCGAGCCCTA
        b          K   K   A   K   K   G   K   E   M   A   R   M   N   T   R   L   K   L   G   I   -

                 AACGGACCTGCTCGAGGACATCGGCGCTGAGGACGACGAGAGCGTGCTCATCACGCTCGT
        1741     --------+---------+---------+---------+---------+---------+  1800
                 TTGCCTGGACGAGCTCCTGTAGCCGCGACTCCTGCTGCTCTCGCACGAGTAGTGCGAGCA
        b          T   D   L   L   E   D   I   G   A   E   D   D   E   S   V   L   I   T   L   V   -

                 GCCCAGGAGCGGCAAGGGAATGGTGAAGGTTGGAGGGCTAAGGATTGATTTCTCCAAGTG
        1801     --------+---------+---------+---------+---------+---------+  1860
                 CGGGTCCTCGCCGTTCCCTTACCACTTCCAACCTCCCGATTCCTAACTAAAGAGGTTCAC
        b          P   R   S   G   K   G   M   V   K   V   G   G   L   R   I   D   F   S   K   *   -

                 ATGAGCATATTGTGAAGAGAAAATTTGCATTTACCGCCCTATAGAATCGAAAAATTGCGT
        1861     --------+---------+---------+---------+---------+---------+  1920
                 TACTCGTATAACACTTCTCTTTTAAACGTAAATGGCGGGATATCTTAGCTTTTTAACGCA
        b          *   A   Y   C   E   E   K   I   C   I   Y   R   P   I   E   S   K   N   C   V   -

                 ATATGTCCCATTATTGTTTTTTTTTATTCTTCAAGCGTATTCAGAATAAGAGTTGCGTGCA
        1921·    --------+---------+---------+---------+---------+---------+  1980
                 TATACAGGGTAATAACAAAAAAAATAAGAAGTTCGCATAAGTCTTATTCTCAACGCACGT
        b          Y   V   P   L   L   F   F   L   F   F   K   R   I   Q   N   K   S   C   V   H   -

                 TGCACGCATGCAGCCATGTTGTTGTAGTCGATATGTGGGGTATGTTTGGATCAGGGATAA
        1981     --------+---------+---------+---------+---------+---------+  2040
                 ACGTGCGTACGTCGGTACAACAACATCAGCTATACACCCCATACAAACCTAGTCCCTATT
        b          A   R   M   Q   P   C   C   C   S   R   Y   V   G   Y   V   W   I   R   D   N   -

                 TGATGTGAACTTTGAATTAATTATTACACTCTTGAGAATAAATTAGAGAGTTTATTATGCA
        2041     --------+---------+---------+---------+---------+---------+  2100
                 ACTACACTTGAAACTTAATTAATAATGTGAGACTCTTATTTAATCTCTCAAATAATACGT
        b          D   V   N   F   E   L   I   I   T   L   *   E   *   I   R   E   F   I   M   Q   -

                 AGTTGCTTGGTGTAATAGATATTCAACATTGTTTCCTATACATCTTTTTTTGGAAGAAAA
        2101     --------+---------+---------+---------+---------+---------+  2160
                 TCAACGAACCACATTATCTATAAGTTGTAACAAAGGATATGTAGAAAAAAACCTTCTTTT
        b          V   A   W   C   N   R   Y   S   T   L   P   P   I   H   L   F   L   E   E   K

                 AAAAAAAAAAAAAAAAATCGAT
        2161     --------+---------+-  2181
                 TTTTTTTTTTTTTTTTTAGCTA
        b          K   K   K   K   K   S   -
```

FIGURE 10-3

```
          CACGCCACCCTTCTCTCTCTCTCTCTCTCTGGTCTACTGAACAGTAATAGACATGTCCCT
  1       ---------+---------+---------+---------+---------+---------+   60
          GTGCGGTGGGAAGAGAGAGAGAGAGAGAGACCAGATGACTTGTCATTATCTGTACAGGGA
           T  P  P  F  S  L  S  L  S  L  V  Y  *  T  V  I  D  M  S  L  -

          GCTGTTGAACTCTAGCTTCACCGGTGCTTCCTCTGCATGCCTCCTCCAACGGGAAAGGTC
  61      ---------+---------+---------+---------+---------+---------+   120
          CGACAACTTGAGATCGAAGTGGCCACGAAGGAGACGTACGGAGGAGGTTGCCCTTTCCAG
           L  L  N  S  S  F  T  G  A  S  S  A  C  L  L  Q  R  E  R  S  -

          CCGCCGCCGCCGCCTCCACGTCCCTGGCGTGACATGCCGCCAGGGCAGTAATGGTGACCG
  121     ---------+---------+---------+---------+---------+---------+   180
          GGCGGCGGCGGCGGAGGTGCAGGGACCGCACTGTACGGCGGTCCCGTCATTACCACTGGC
           R  R  R  R  L  H  V  P  G  V  T  C  R  Q  G  S  N  G  D  R  -

          CAGAGATGCCGCCCCCCAGCAGCAGTCGCCGCCGCTGCTGGATCGGCGCGACATGCTGTT
  181     ---------+---------+---------+---------+---------+---------+   240
          GTCTCTACGGCGGGGGGTCGTCGTCAGCGGCGGCGACGACCTAGCCGCGCTGTACGACAA
           R  D  A  A  P  Q  Q  Q  S  P  P  L  L  D  R  R  D  M  L  L  -

          GGCTTTAGGAGGGCTTTACGGCCTGACCGCAGGACCCAAGGTTCTGGCGGCGCCGATAAT
  241     ---------+---------+---------+---------+---------+---------+   300
          CCCAAATCCTCCCGAAATGCCGCACTGGCGTCCTGGGTTCCAAGACCGCCGCGGCTATTA
           G  L  G  G  L  Y  G  V  T  A  G  P  K  V  L  A  A  P  I  M  -

          GCCGCCGGATCTGTCCAAGTGCTACCCTGCCACCGCACCTGCCCTCGACAACAAATGCTG
  301     ---------+---------+---------+---------+---------+---------+   360
          CGGCGGCCTAGACAGGTTCACGATGGGACGGTGGCGTGGACGGGAGCTGTTGTTTACGAC
           P  P  D  L  S  K  C  Y  P  A  T  A  P  A  L  D  N  K  C  C  -

          CCCGCCTTACGACCCCGGCGAGACGATCTCGCAGTACAGCTTCCCTGCTACGCCCCTCCG
  361     ---------+---------+---------+---------+---------+---------+   420
          GGGCGGAATGCTGGGGCCGCTCTGCTAGAGCCTCATGTCGAAGGGACGATGCGGGGAGGC
           P  P  Y  D  P  G  E  T  I  S  E  Y  S  F  P  A  T  P  L  R  -

          GGTGCGGCGGCCGGCCCCATATCGTGAAGGACGATCAGGAGTATATGGACAAGTACAAGGA
  421     ---------+---------+---------+---------+---------+---------+   480
          CCACGCCGCCGGCCGGGTATAGCACTTCCTGCTAGTCCTCATATACCTGTTCATGTTCCT
           V  R  R  P  A  H  I  V  K  D  D  Q  E  Y  M  D  K  Y  R  E  -

          GGCAGTGAGGAGGATGAAGAATCTGCCGGCAGACCACCCTTGGAACTACTACCAGCAGGC
  481     ---------+---------+---------+---------+---------+---------+   540
          CCGTCACTCCTCCTACTTCTTAGACGGCCGTCTGGTGGGAACCTTGATGATGGTCGTCCG
           A  V  R  R  M  K  N  L  P  A  D  H  P  W  N  Y  Y  Q  Q  A  -

          GAACATCCACTGCCAGTATTGCAACTACGCCTACCACCAGCAAAATACCGACGACGTGCC
  541     ---------+---------+---------+---------+---------+---------+   600
          CTTGTAGGTGACGGTCATAACGTTGATGCGGATGGTGGTCGTTTTATGGCTGCTGCACGG
           N  I  H  C  Q  Y  C  N  Y  A  Y  H  Q  Q  N  T  D  D  V  P  -

          CATCCACGTCCACTTCAGCTGGATCTTCCTCCCATGGCACCGCTACTACCTCCACTTCTA
  601     ---------+---------+---------+---------+---------+---------+   660
          GTAGGTCCAGGTGAAGTCGACCTAGAAGGAGGGTACCGTGGCGATGATGGAGGTGAAGAT
           I  Q  V  H  F  S  W  I  F  L  P  M  H  R  Y  Y  L  H  F  Y  -

          CGAAAGGATCCTCGGCAAGCTCATCGACGACGACACCTTCACCATCCCATTCTGGAACTG
  661     ---------+---------+---------+---------+---------+---------+   720
          GCTTTCCTAGGAGCCGTTCGAGTAGCTGCTGCTCTGGAAGTGGTAGGGTAAGACCTTGAC
           E  R  I  L  G  K  L  I  D  D  D  T  F  T  I  P  F  W  N  W  -

          CGACACCAAGGACGGGATGACGTTCCCCGCCATCTTCCAGGATGCGGCATCCCCGCTGTA
  721     ---------+---------+---------+---------+---------+---------+   780
          CCTGTGGTTCCTGCCCTACTGCAAGGGGCGGTAGAAGGTCCTACGCCGTAGGGGCGACAT
           D  T  K  D  G  M  T  F  P  A  I  F  Q  D  A  A  S  P  L  Y  -

          CGACCCGAGACGCGACCAACGCCACGTCAAGGACGGTAAGATCCTCGACCTCAAGTACGC
  781     ---------+---------+---------+---------+---------+---------+   840
          GCTGGGCTCTGCGCTGGTTGCGGTGCAGTTCCTGCCGTTCTAGGAGCTGGAGTTCATGCG
           D  P  R  R  D  Q  R  H  V  K  D  G  K  I  L  D  L  K  Y  A  -
```

FIGURE 11-1

```
         CTACACCGAAAACACTGCATCCGACAGCGAGATCATACGGGAGAACCTCTGCTTCATACA
   841   -------------------+---------+---------+---------+----------+   900
         GATGTGGCTTTTGTGACGTAGGCTGTCGCTCTAGTATGCCCTCTTGGAGACGAAGTATGT
          Y  T  E  N  T  A  S  D  S  E  I  I  R  E  N  L  C  F  I  Q   -

         GAAGACCTTCAAGCACAGCCTGTCGCTGGCGGAACTGTTCATGGGGGATCCCGTGCGCGC
   901   -------------------+---------+---------+---------+----------+   960
         CTTCTGCAAGTTCGTGTCGGACAGCGACCGCCTTGACAAGTACCCCCTAGGGCACGCGCG
          K  T  F  K  H  S  L  S  L  A  E  L  F  M  G  D  P  V  R  A   -

         GGGGGAGAAGGAGATCCAGGAGGCTAATGGGCAGATGGAAGTCATCCACAATGCGGCGCA
   961   -------------------+---------+---------+---------+----------+  1020
         CCCCCTCTTCCTCTAGGTCCTCCGATTACCCGTCTACCTTCAGTAGGTGTTACGCCGCGT
          G  E  K  E  I  Q  E  A  N  G  Q  M  E  V  I  H  N  A  A  H   -

         CATGTGGGTCGGAGAGCCGGACGCATACAAGGAAAACATGGGGGACTTCTCCACCGCCGC
  1021   -------------------+---------+---------+---------+----------+  1080
         GTACACCCAGCCTCTCGGCCTGCCTATGTTCCTTTTGTACCCCCTGAAGAGGTGGCGGCG
          M  W  V  G  E  P  D  G  Y  K  E  N  M  G  D  F  S  T  A  A   -

         CCGCGATTCTGTTTTCTTCTGCCACCATTCCAATGTCGACCGCATGTGGGACATCTACCG
  1081   -------------------+---------+---------+---------+----------+  1140
         GGCGCTAAGACAAAAGAAGACGGTGGTAAGGTTACAGCTGGCGTACACCCTGTAGATGGC
          R  D  S  V  F  F  C  H  H  S  N  V  D  R  M  W  D  I  Y  R   -

         CAACCTCCGCGGCAACCGCGTCGAGTTCGAAGACAACGACTGGTTGGACAGCACCTTCCT
  1141   -------------------+---------+---------+---------+----------+  1200
         GTTGGAGGCGCCGTTGGCGCAGCTCAAGCTTCTGTTGCTGACCAACCTGTCGTGGAAGGA
          N  L  R  G  N  R  V  E  F  E  D  N  D  W  L  D  S  T  F  L   -

         CTTCCACGACGAGAACGAACAGCTCGTCAAAGTCAAGATGAGCGACTGCCTCAACCCGAC
  1201   -------------------+---------+---------+---------+----------+  1260
         GAAGGTGCTGCTCTTGCTTGTCGAGCAGTTTCAGTTCTACTCGCTGACGGAGTTGGGCTG
          F  H  D  E  N  E  Q  L  V  K  V  K  M  S  D  C  L  N  P  T   -

         CAAGCTTCGGTACACGTTCGAGCAAGTTCCCCTCCCATGGCTGGGCAAAATCAATTGCCA
  1261   -------------------+---------+---------+---------+----------+  1320
         GTTCGAAGCCATGTGCAAGCTCGTTCAAGGGGAGGGTACCGACCCGTTTTAGTTAACGGT
          K  L  R  Y  T  F  E  Q  V  P  L  P  W  L  G  K  I  N  C  Q   -

         GAAGACGGCAGAGACGAAGTCCAAGGCCACGACGGAGCTGTCGCTGACGCGCGTGAACGA
  1321   -------------------+---------+---------+---------+----------+  1380
         CTTCTGCCGTCTCTGCTTCAGGTTCCGGTGCTGCCTCGACAGCGACTGCGCGCACTTGCT
          K  T  A  E  T  K  S  K  A  T  T  E  L  S  L  T  R  V  N  E   -

         ATTCGGGACGACGGCCCAGGCACTCGACGCGAGCAACCCGCTGCGGGTGATCGTGGCAAG
  1381   -------------------+---------+---------+---------+----------+  1440
         TAAGCCCTGCTGCCGGGTCCGTGAGCTGCGCTCGTTGGGCGACGCCCACTAGCACCGTTC
          F  G  T  T  A  Q  A  L  D  A  S  N  P  L  R  V  I  V  A  R   -

         GCCGAAGAAGAACCGCAAGAAGAAGGAGAAGCAAGAGAAGGTGGGGGTGATTCAGATCAA
  1441   -------------------+---------+---------+---------+----------+  1500
         CGGCTTCTTCTTGGCGTTCTTCTTCCTCTTCGTTCTCTTCCACCCCACTAAGTCTAGTT
          P  K  K  N  R  K  K  K  E  K  Q  E  K  V  G  V  I  Q  I  K   -

         GGATATTAAGGTGACCACCAACGAGACAGCTCGCTTCGACGTCTATGTCGCCGGTTCCTTA
  1501   -------------------+---------+---------+---------+----------+  1560
         CCTATAATTCCACTGGTGGTTGCTCTGTCGAGCGAAGCTGCAGATACAGCGCCAAGGAAT
          D  I  K  V  T  T  N  E  T  A  R  F  D  V  Y  V  A  V  P  Y   -

         CGGTGACCTCGCCGGACCCGACTACGGCGAGTTCGCGGGCAGCTACGTGAGGCTGGCGCA
  1561   -------------------+---------+---------+---------+----------+  1620
         GCCACTGGAGCGGCCTGGGCTGATGCCGCTCAAGCGCCCGTCGATGCACTCCGACCGCGT
          G  D  L  A  G  P  D  Y  G  E  F  A  G  S  Y  V  R  L  A  H   -

         TAGGATGAAGGGAAGCGACGGGACCGAAAAGCAGGGCCCAAGAAGAAGGGAAAACTCAA
  1621   -------------------+---------+---------+---------+----------+  1680
         ATCCTACTTCCCTTCGCTGCCCTGGCTTTTCGTCCCGGGTTCTTCTTCCCTTTTGAGTT
          R  M  K  G  S  D  G  T  E  K  Q  G  P  R  R  R  G  K  L  K   -
```

<p align="center">FIGURE 11-2</p>

```
        GCTGGGTATTACGCCGCTGCTCGAGGACATCGATGCTGAGGACGCCGACAAGTTGGTGGT
1681    ------------+---------+---------+---------+---------+---------+ 1740
        CGACCCATAATGCGGCGACGAGCTCCTGTAGCTACGACTCCTGCGGCTGTTCAACCACCA
         .L  G  I  T  P  L  L  E  D  I  D  A  E  D  A  D  K  L  V  V  -

        CACCCTGGTTCTCCGCACTGGGAGCGTCACCGTGGGGGGAGTTTCCATCAATCTCCTGCA
1741    ------------+---------+---------+---------+---------+---------+ 1800
        GTGGGACCAAGAGGCGTGACCCTCGCAGTGGCACCCCCCTCAAAGGTAGTTAGAGGACGT
          T  L  V  L  R  T  G  S  V  T  V  G  G  V  S  I  N  L  L  Q  -

        GACAGATTCTACCGCCGCCATCTAAATGATGGCCTCGGATCACAGCTTCTCCCCGCTTAA
1801    ---------+---------+---------+---------+---------+---------+ 1860
        CTGTCTAAGATGGCGGCGGTAGATTTACTACCGGAGCCTAGTGTCGAAGAGGGGCGAATT
          T  D  S  T  A  A  I  *

        GTTGGAGTGATCGATTACTGGTGCTGCTTTCTTCCTCCCTGTCGTTCTTGCTATCTTCTT
1861    ---------+---------+---------+---------+---------+---------+ 1920
        CAACCTCACTAGCTAATGACCACGACGAAAGAAGGAGGGACAGCAAGAACGATAGAAGAA

        GATCTGGAACGATCCTTCAATAATTAGGGCATGACAGTAGTCGTCGCCCGATCCCATATG
1921    ---------+---------+---------+---------+---------+---------+ 1980
        - CTAGACCTTGCTAGGAAGTTATTAATCCCGTACTGTCATCAGCAGCGGGCTAGGGTATAC

        TACGTGTTGGTCTCAACAGCTGTACATGTGACGTTATGGTGTGACTATATATTTTATTGC
1981    ---------+---------+---------+---------+---------+---------+ 2040
        ATGCACAACCAGAGTTGTCGACATGTACACTGCAATACCACACTGATATATAAAATAACG

        GGTCATCCTTGTTTCTTTCTTAAAAAAAAAAAAAAAAAA
2041    ---------+---------+---------+--------- 2078
        CCAGTAGGAACAAAGAAAGAATTTTTTTTTTTTTTTTTTT
```

FIGURE 11-3

```
      AATGTGGATCGGATGTGGACGGTGTGGAAGAAGCTGCACGGCGACAAGCCGGAGTTCGTC
  1   --------+---------+---------+---------+---------+---------+  60
      TTACACCTAGCCTACACCTGCCACACCTTCTTCGACGTGCCGCTGTTCGGCCTCAAGCAG
       N  V  D  R  M  W  T  V  W  K  K  L  H  G  D  K  P  E  F  V   -


      GACCAGGAGTGGCTCGAGTCTGAATTCACCTTCTACGACGAGAATGTGCGCCTGCGCAGG
  61  --------+---------+---------+---------+---------+---------+  120
      CTGGTCCTCACCGAGCTCAGACTTAAGTGGAAGATGCTGCTCTTACACGCGGACGCGTCC
       D  Q  E  W  L  E  S  E  F  T  F  Y  D  E  N  V  R  L  R  R   -


      ATCAAGGTGCGCGACGTGTTGAACATAGACAAACTCAGGTACCGGTACGAAGACATCGAC
 121  --------+---------+---------+---------+---------+---------+  180
      TAGTTCCACGCGCTGCACAACTTGTATCTGTTTGAGTCCATGGCCATGCTTCTGTAGCTG
       I  K  V  R  D  V  L  N  I  D  K  L  R  Y  R  Y  E  D  I  D   -


      ATGCCATGGCTCGCTGCACGTCCCAAGCCTTCCGTTCACCCTAAGATCGCGCGCGACATA
 181  --------+---------+---------+---------+---------+---------+  240
      TACGGTACCGAGCGACGTGCAGGGTTCGGAAGGCAAGTGGGATTCTAGCGCGCGCTGTAT
       M  P  W  L  A  A  R  P  K  P  S  V  H  P  K  I  A  R  D  I   -


      TTGAAGAAGCGTAATGGCGAAGGCGTACTGAGAATGCCCGGCGAAACGGATCGTTCACAA
 241  --------+---------+---------+---------+---------+---------+  300
      AACTTCTTCGCATTACCGCTTCCGCATGACTCTTACGGGCCGCTTTGCCTAGCAAGTGTT
       L  K  K  R  N  G  E  G  V  L  R  M  P  G  E  T  D  R  S  Q   -


      CTCTCCGAAGATGGTAGCTGGACACTGGACAAGAGCATCACCGTGAGGGTTGACAGGCCA
 301  --------+---------+---------+---------+---------+---------+  360
      GAGAGGCTTCTACCATCGACCTGTGACCTGTTCTCGTAGTGGCACTCCCAACTGTCCGGT
       L  S  E  D  G  S  W  T  L  D  K  S  I  T  V  R  V  D  R  P   -


      AGGATCAACAGGACAGGGCAAGAAAAAGAGGAAGAAGAGGAGATCTTATTGGTCTACGGA
 361  --------+---------+---------+---------+---------+---------+  420
      TCCTAGTTGTCCTGTCCCGTTCTTTTTCTCCTTCTTCTCCTCTAGAATAACCAGATGCCT
       R  I  N  R  T  G  Q  E  K  E  E  E  E  I  L  L  V  Y  G   -


      ATCGATACTAAGAGAAGCAGATTCGTCAAATTCGATGTGTTCATCAACGTCGTCGACGAA
 421  --------+---------+---------+---------+---------+---------+  480
      TAGCTATGATTCTCTTCGTCTAAGCAGTTTAAGCTACACAAGTAGTTGCAGCAGCTGCTT
       I  D  T  K  R  S  R  F  V  K  F  D  V  F  I  N  V  V  D  E   -


      ACCGTGCTGAACCCAAAGTCGAGGGAGTTCGCAGGGACCTTCGTCAATCTCCACCACGTC
 481  --------+---------+---------+---------+---------+---------+  540
      TGGCACGACTTGGGTTTCAGCTCCCTCAAGCGTCCCTGGAAGCAGTTAGAGGTGGTGCAG
       T  V  L  N  P  K  S  R  E  F  A  G  T  F  V  N  L  H  H  V   -


      TCGAGGACGAAAAGCCATGAGGATGGCGGCGTGGGTTCGAAGATGAAAAGCCACCTTAAG
 541  --------+---------+---------+---------+---------+---------+  600
      AGCTCCTGCTTTTCGGTACTCCTACCGCCGCACCCAAGCTTCTACTTTTCGGTGGAATTC
       S  R  T  K  S  H  E  D  G  G  V  G  S  K  M  K  S  H  L  K   -


      CTCGGTATATCGGAACTTTTGGAAGACCTCGAGGCAGACGAAGATGATTGCATCTGGGTG
 601  --------+---------+---------+---------+---------+---------+  660
      GAGCCATATAGCCTTGAAAACCTTCTGGAGCTCCGTCTGCTTCTACTAACGTAGACCCAC
       L  G  I  S  E  L  L  E  D  L  E  A  D  E  D  D  C  I  W  V   -


      ACACTGGTGCCAAGAGGCGGCACGGGGGTCAACACCACCGTAGACGGCGTCCGGATCGAC
 651  --------+---------+---------+---------+---------+---------+  720
      TGTGACCACGGTTCTCCGCCGTGCCCCCAGTTGTGGTGGCATCTGCCGCAGGCCTAGCTG
       T  L  V  P  R  G  G  T  G  V  N  T  T  V  D  G  V  R  I  D   -


      TACATGAAGTAGTGAACCGGCACGCCGCTCCTCCCCTCCCCATCAGAAGTGGTATAATAT
 721  --------+---------+---------+---------+---------+---------+  750
      ATGTACTTCATCACTTGGCCGTGCGGCGAGGAGGGGAGGGGTAGTCTTCACCATATTATA
       Y  M  K  -
```

FIGURE 12-1

```
       TTATATTGGATCGAGGCTCGTGGTATCTTTTGATAAGAGTAAGTTCCATAAATTTAGAAG
781    --------+---------+---------+---------+---------+---------+  840
       AATATAACCTAGCTCCGAGCACCATAGAAAACTATTCTCATTCAAGGTATTTAAATCTTC

       AAGAATCATGTTCTTTATTTATATTAAATCAATGTGATTTGTCCAAAAAAAAAAAAAAAAA
841    --------+---------+---------+---------+---------+---------+  900
       TTCTTAGTACAAGAAATAAATATAATTTAGTTACACTAAACAGGTTTTTTTTTTTTTTTTT
```

FIGURE 12-2

```
        TGCACTGTGCGTATTGCGACGGCGCGTATGACCAAATCGGCTTCCCCGATCTCGAGATCC
    1   --------+---------+---------+---------+---------+---------+   60
        ACGTGACACGCATAACGCTGCCGCGCATACTGGTTTAGCCGAAGGGGCTAGAGCTCTAGG
c         H  C  A  Y  C  D  G  A  Y  D  Q  I  G  F  P  D  L  E  I  Q  -

        AGATCCACAACTCGTGGCTCTTCTTTCCTTGGCACCGGTTCTACCTCTACTCCAACGAGC
   61   --------+---------+---------+---------+---------+---------+  120
        TCTAGGTGTTGAGCACCGAGAAGAAAGGAACCGTGGCCAAGATGGAGATGAGGTTGCTCG
c         I  H  N  S  W  L  F  F  P  W  H  R  P  Y  L  Y  S  N  E  R  -

        GCATACTCGGGAAACTTATCGGCGACGACACGTTCGCGCTGCCTTTCTGGAACTGGGACG
  121   --------+---------+---------+---------+---------+---------+  180
        CGTATGAGCCCTTTGAATAGCCGCTGCTGTGCAAGCGCGACGGAAAGACCTTGACCCTGC
c         I  L  G  K  L  I  G  D  D  T  F  A  L  P  P  W  N  W  D  A  -

        CGCCGGGGGGCATGCAGTTCCCGTCTATCTACACGGACCCTTCATCCTCGCTATATGACA
  181   --------+---------+---------+---------+---------+---------+  240
        GCGGCCCCCCGTACGTCAAGGGCAGATAGATGTGCCTGGGAAGTAGGAGCGATATACTGT
c         P  G  G  M  Q  F  P  S  I  Y  T  D  P  S  S  S  L  Y  D  K  -

        AGCTGCGTGATGCGAAGCACCAGCCGCCGACTTTGATTGACCTCGACTACAATGGCACCG
  241   --------+---------+---------+---------+---------+---------+  300
        TCGACGCACTACGCTTCGTGGTCGGCGGCTGAAACTAACTGGAGCTGATGTTACCGTGGC
c         L  R  D  A  K  H  Q  P  P  T  L  I  D  L  D  Y  N  G  T  D  -

        ATCCTACCTTCTCCCCTGAAGAACAGATTAACCACAACCTCGCCGTCATGTACCGACAGG
  301   --------+---------+---------+---------+---------+---------+  360
        TAGGATGGAAGAGGGGACTTCTTGTCTAATTGGTGTTGGAGCGGCAGTACATGGCTGTCC
c         P  T  F  S  P  E  E  Q  I  N  H  N  L  A  V  M  Y  R  Q  V  -

        TGATATCCAGTGGAAAGACACCAGAGCTGTTTATGGGCTCAGCGTACCGCGCCGGTGACC
  361   --------+---------+---------+---------+---------+---------+  420
        -ACTATAGGTCACCTTTCTGTGGTCTCGACAAATACCCGAGTCGCATGGCGCGGCCACTGG
c         I  S  S  G  K  T  P  E  L  F  M  G  S  A  Y  R  A  G  D  Q  -

        AGCCTGACCCCGGCGCAGGCTCTGTAGAGCAGAAGCCGCACGGCCCGGTGCATGTGTGGA
  421   --------+---------+---------+---------+---------+---------+  480
        TCGGACTGGGGCCGCGTCCGAGACATCTCGTCTTCGGCGTGCCGGGCCACGTACACACCT
c         P  D  P  G  A  G  S  V  E  Q  K  P  H  G  P  V  H  V  W  T  -

        CAGGTGATCGCAACCAGCCCAATCGCGAAGACATGGGCACGCTCTACTCGGCGGCGTGGG
  481   --------+---------+---------+---------+---------+---------+  540
        GTCCACTAGCGTTGGTCGGGTTAGCGCTTCTGTACCCGTGCGAGATGAGCCGCCGCACCC
c         G  D  R  N  Q  P  N  R  E  D  M  G  T  L  Y  S  A  A  W  D  -

        ACCCCGTCTTCTTCGCACACCACGGCAACATCGACCGCATGTGGTACGTGTGGAGGAACC
  541   --------+---------+---------+---------+---------+---------+  600
        TGGGGCAGAAGAAGCGTGTGGTGCCGTTGTAGCTGGCGTACACCATGCACACCTTCTTGG
c         P  V  F  F  A  H  H  G  N  I  D  R  M  W  Y  V  W  R  N  L  -

        TTGGCGGCAAGCACCGCAACTTCACCGACCCCGACTGGCTCAACGCGTCCTTCCTGTTCT
  601   --------+---------+---------+---------+---------+---------+  660
        AACCGCCGTTCGTGGCGTTGAAGTGGCTGGGGCTGACCGAGTTGCGCAGGAAGGACAAGA
c         G  G  K  H  R  N  F  T  D  P  D  W  L  N  A  S  F  L  F  Y  -

        ATGATGAGAATGCGCAGCTCGTCCGTGTTAAAGTAAAAGACTGCTTAGAGGCCGACGCAA
  661   --------+---------+---------+---------+---------+---------+  720
        TACTACTCTTACGCGTCGAGCAGGCACAATTTCATTTTCTGACGAATCTCCGGCTGCGTT
c         D  E  N  A  Q  L  V  R  V  K  V  K  D  C  L  E  A  D  A  M  -

        TGCGGTACACATACCAGGATGTAGAGATCCCGTGGCTCAAAGCAAAGCCGACGCCAAAGA
  721   --------+---------+---------+---------+---------+---------+  780
        ACGCCATGTGTATGGTCCTACATCTCTAGGGCACCGAGTTTCGTTTCGGCTGCGGTTTCT
c         R  Y  T  Y  Q  D  V  E  I  P  W  L  K  A  K  P  T  P  K  S  -
```

FIGURE 13-1

```
        GCGCCCTACAGAAGATAAAGAGCAAGGTATCGACGCTGAAGGCAACACCAAGGGGGACGA
   781  ---------+---------+---------+---------+---------+---------+  840
        CGCGGGATGTCTTCTATTTCTCGTTCCATAGCTGCGACTTCCGTTGTGGTTCCCCCTGCT
  c      A  L  Q  K  I  K  S  K  V  S  T  L  K  A  T  P  R  G  T  T -

        CGACTACCACAGCAGAGACTACATTTCCGGTGGTGCTGGATAAGCCGGTGAGTGCAACAG
   841  ---------+---------+---------+---------+---------+---------+  900
        GCTGATGGTGTCGTCTCTGATGTAAAGGCCACCACGACCTATTCGGCCACTCACGTTGTC
  c      T  T  T  A  E  T  T  F  P  V  V  L  D  K  P  V  S  A  T  V -

        TGGCTAGACCGAAGGCCAGGAGGAGTGGGAAGGAGAAGGAAGAAGAGGAGGAGGTGTTGG
   901  ---------+---------+---------+---------+---------+---------+  960
        ACCGATCTGGCTTCCGGTCCTCCTCACCCTTCCTCTTCCTTCTTCTCCTCCTCCACAACC
  c      A  R  P  K  A  R  R  S  G  K  E  K  E  S  E  E  E  V  L  V -

        TGGTGGAGGGAATCGAGTTGGAGAAGGACGTGTTCGTGAAGTTTGATGTGTATATAAACT
   961  ---------+---------+---------+---------+---------+---------+  1020
        ACCACCTCCCTTAGCTCAACCTCTTCCTGCACAAGCACTTCAAACTACACATATATTTGA
  c      V  E  G  I  E  L  E  K  D  V  F  V  K  F  D  V  Y  I  N  S -

        CGCCCGGAGCACGAAGGGGTGGGGCCCGGCAGGCGAGTGAGTTCGCAGGGAGCTTCGTCCACG
  1021  ---------+---------+---------+---------+---------+---------+  1080
        GCGGGCCTCGTGCTTCCCCACCCCCGGCCTCCGCTCACTCAAGCGTCCCTCGAAGCAGGTGC
  c      P  E  H  E  G  V  G  P  E  A  S  E  F  A  G  S  F  V  H  V -

        TGCCACACAAGCACAAGAAGGCGAAGAAGGGGAAGGAGATGGCCAGGATGAACACAAGGC
  1081  ---------+---------+---------+---------+---------+---------+  1140
        ACGGTGTGTTCGTGTTCTTCCGCTTCTTCCCCTTCCTCTACCGGTCCTACTTGTGTTCCG
  c      P  H  K  H  K  K  A  K  K  G  K  E  M  A  R  M  N  T  R  L -

        TTAAGCTCGGGATAACGGACCTGCTCGAGGACATCGGCGCTGAGGACGACGAGAGCGTGC
  1141  ---------+---------+---------+---------+---------+---------+  1200
        AATTCGAGCCCTATTGCCTGGACGAGCTCCTGTAGCCGCGACTCCTGCTGCTCTCGCACG
  c      K  L  G  I  T  D  L  L  E  D  I  G  A  E  D  D  E  S  V  L -

        TCATCACGCTCGTGCCCAGGAGCGGCAAGGGAATGGTGAAGGTTGGAGGGCTAAGGATTG
  1201  ---------+---------+---------+---------+---------+---------+  1260
        AGTAGTGCGAGCACGGGTCCTCGCCGTTCCCTTACCACTTCCAACCTCCCGATTCCTAAC
  c      I  T  L  V  P  R  S  G  K  G  M  V  K  V  G  G  L  R  I  D -

        ATTTCTCCAAGTGATGAGCATATTGTGAAGAGAAAATTTGCATTTACCGCCCTATAGAAT
  1261  ---------+---------+---------+---------+---------+---------+  1320
        TAAAGAGGTTCACTACTCGTATAACACTTCTCTTTTAAACGTAAATGGCGGGATATCTTA
  c      F  S  K  *  *  A  Y  C  E  E  K  I  C  I  Y  R  P  I  E  S -

        CGAAAAAATTGCGTATATGTCCCATTATTGTTTTTTTTTATTCTTCAAGCGTATTCAGAATA
  1321  ---------+---------+---------+---------+---------+---------+  1380
        GCTTTTTAACGCATATACAGGGTAATAACAAAAAAAAATAAGAAGTTCGCATAAGTCTTAT
  c      K  N  C  V  Y  V  P  L  L  F  L  F  F  K  R  I  Q  N  K -

        AGAGTTGCGTGCATGCACGCATGCAGCCATGTTGTTGTAGTCGATATGTGGGTATGTTT
  1381  ---------+---------+---------+---------+---------+---------+  1440
        TCTCAACGCACGTACGTGCGTACGTCGGTACAACAACATCAGCTATACACCCCATACAAA
  c      S  C  V  H  A  R  H  Q  P  C  C  C  S  R  Y  V  G  Y  V  W -

        GGATCAGGGATAATGATGTGAACTTTGAATTAATTATTACACTCTGAGAATAAATTAGAG
  1441  ---------+---------+---------+---------+---------+---------+  1500
        CCTAGTCCCTATTACTACACTTGAAACTTAATTAATAATGTGAGACTCTTATTTAATCTC
  c      I  R  D  N  D  V  N  F  E  L  I  I  T  L  *  E  *  I  R  E -

        AGTTTATTATGCAAAAAAAAAA
  1501  ---------+---------+--  1522
        TCAAATAATACGTTTTTTTTTT
  c      F  I  M  Q  K  K      -
```

FIGURE 13-2

```
      ACAACAAACCAGTGCCTGGTTTAGGTGTATTCACTATGGCCACCCTCTCTAAACTAGCTT
    1 ---------+---------+---------+---------+---------+---------+ 60
      TGTTGTTTGGTCACGGACCAAATCCACATAAGTGATACCGGTGGGAGAGATTTGATCGAA
  c      N   K   P   V   P   G   L   G   V   F   T   M   A   T   L   S   K   L   A   S  -

      CCCCAACCAATAACACCTCCACTCTCCCCGCTCCCTCCTTTGCATGCTCCTTCTCTCACC
   61 ---------+---------+---------+---------+---------+---------+ 120
      GGGGTTGGTTATTGTGGAGGTGAGAGGGGCGAGGGAGGAAAACGTACGAGGAAGAGAGTGG
  c      P   T   N   N   T   S   T   L   P   A   P   S   P   A   C   S   F   S   H   Q  -

      AAAAGCTTCACCACCACCTTCCTCTCCCCTGTAGGGGTCCCAAACCACCCCGTCATAAGA
  121 ---------+---------+---------+---------+---------+---------+ 180
      TTTTCGAAGTGGTGGTGGAAGGAGAGGGGACATCCCCAGGGTTTGGTGGGGCAGTATTCT
  c      K   L   H   H   H   L   P   L   P   C   R   G   P   K   P   P   R   H   K   I  -

      TCTCATGCAAATCTAAGGAGCAACAAGAGAATGCCGACAAGCCTGCGGGCCGCATCGACC
  181 ---------+---------+---------+---------+---------+---------+ 240
      AGAGTACGTTTAGATTCCTCGTTGTTCTCTTACGGCTGTTCGGACGCCCGGCGTAGCTGG
  c      S   C   K   S   K   E   Q   Q   E   N   A   D   K   P   A   G   R   I   D   R  -

      GCCGCGACCTACTCCTGGGCCTCGGCGGGCTTTACGGTGCCACCACTGGGCTCGGCCTCA
  241 ---------+---------+---------+---------+---------+---------+ 300
      CGGCGCTGGATGAGGACCCGGAGCCGCCCGAAATGCCACGGTGGTGACCCGAGCCGGAGT
  c      R   D   L   L   L   G   L   G   G   L   Y   G   A   T   T   G   L   G   L   N  -

      ACCGTCGAGCGGCCGCCGCCCCTATCCTGGCTCCCGACCTCTCAACTTGTGGGCCGCCTG
  301 ---------+---------+---------+---------+---------+---------+ 360
      TGGCAGCTCGCCGGCGGCGGGGATAGGACCGAGGGCTGGAGAGTTGAACACCCGGCGGAC
  c      R   R   A   A   A   A   P   I   L   A   P   D   L   S   T   C   G   P   P   A  -

      CCGACCTCCCTGCCTCCGCCCGACCGACAGTTTGCTGCCCGCCATACCAATCCACCATCA
  361 ---------+---------+---------+---------+---------+---------+ 420
      GGCTGGAGGGACGGAGGCGGGCTGGCTGTCAAACGACGGGCGGTATGGTTAGGTGGTAGT
  c      D   L   P   A   S   A   R   P   T   V   C   C   P   P   Y   Q   S   T   I   I  -

      TCGTCTTCAAGCTCCCCCCGCGATCTGCTCCGCTTCGCGTCCGGCCTGCGGCCCACTTGG
  421 ---------+---------+---------+---------+---------+---------+ 480
      AGCAGAAGTTCGAGGGGGGCGCTAGACGAGGCGAAGCGCAGGCCGGACGCCGGGTGAACC
  c      V   F   K   L   P   P   R   S   A   P   L   R   V   R   P   A   A   H   L   V  -

      TTGACGCCGACTACCTGGCCAAGTATAAGAAGGCGGTCGAGCTCATGAGGGCCCTGCCGG
  481 ---------+---------+---------+---------+---------+---------+ 540
      AACTGCGGCTGATGGACCGGTTCATATTCTTCCGCCAGCTCGAGTACTCCCGGGACGGCC
  c      D   A   D   Y   L   A   K   Y   K   K   A   V   E   L   M   R   A   L   P   A  -

      CCGACGACCCGCGCAACTTCGTACAGCAAGCGAAAGTGCACTGTGCGTACTGCGACGGCG
  541 ---------+---------+---------+---------+---------+---------+ 600
      GGCTGCTGGGCGCGTTGAAGCATGTCGTTCGCTTTCACGTGACACGCATGACGCTGCCGC
  c      D   D   P   R   N   F   V   Q   Q   A   K   V   H   C   A   Y   C   D   G   A  -

      CGTACGACCAAATCGGCTTCCCCGATCTCGAGATCCAGATCCACAACTCGTGGCTCTTCT
  601 ---------+---------+---------+---------+---------+---------+ 660
      GCATGCTGGTTTAGCCGAAGGGGCTAGAGCTCTAGGTCTAGGTGTTGAGCACCGAGAAGA
  c      Y   D   Q   I   G   F   P   D   L   E   I   Q   I   H   N   S   W   L   F   F  -

      TTCCTTGGCACCGGTTCTACCTCTACTTCAACGAGCGCATACTCGGGAAACTTATCGGTG
  661 ---------+---------+---------+---------+---------+---------+ 720
      AAGGAACCGTGGCCAAGATGGAGATGAAGTTGCTCGCGTATGAGCCCTTTGAATAGCCAC
  c      P   W   H   R   F   Y   L   Y   F   N   E   R   I   L   G   K   L   I   G   D  -

      ACGACACGTTCGCGCTGCCCTTTCTGGAACTGGGACGCGCCGGGGGGGCATGCAGTTCCCGT
  721 ---------+---------+---------+---------+---------+---------+ 780
      TGCTGTGCAAGCGCGACGGAAAGACCTTGACCCTGCGCGGCCCCCCGTACGTCAAGGGCA
  c      D   T   F   A   L   P   F   W   N   W   D   A   P   G   G   H   Q   F   P   S  -
```

FIGURE 14-1

```
       CTATCTACACAGACCCTTCATCCTCGCTATATGACAAGCTGCGTGATGCGAAGCACCAGC
  781  ---------+---------+---------+---------+---------+---------+  840
       GATAGATGTGTCTGGGAAGTAGGAGCGATATACTGTTCGACGCACTACGCTTCGTGGTCG
  c      I  Y  T  D  P  S  S  S  L  Y  D  K  L  R  D  A  K  H  Q  P  -

       CGCCGACTTTGATTGACCTCGACTACAATGGCACA
  841  ---------+---------+---------+----- 875
       GCGGCTGAAACTAACTGGAGCTGATGTTACCGTGT
  c      P  T  L  I  D  L  D  Y  N  G  T  -
```

FIGURE 14-2

```
        GACCACCCATAGATGATGGCTTCTCTCGCCTTGTCTAGTCTTCGCCACCTCCACCACAACC
   1    ------------+---------+---------+---------+---------+---------+   60
        CTGGTGGGTATCTACTACCGAAGAGAGCGGAACAGATCAGAAGGGTGGAGGTGGTGTTGG
                 M  A  S  L  A  L  S  S  L  P  T  S  T  T  T   -

        AAAAAACCCTTATTTTCCAAAACATCCTCGCATGTTAAGCCATTCCATCGCTTCAAAGTT
  61    ------------+---------+---------+---------+---------+---------+  120
        TTTTTTGGGAATAAAAGGTTTTGTAGGAGCGTACAATTCGGTAAGGTAGCGAAGTTTCAA
                 K  K  P  L  F  S  K  T  S  S  H  V  K  P  F  H  R  P  K  V   -

        TCATGCAATGCACCCGCTGATAACAATGACAAAACCGTCAATAATTCTGATACCCCAAAG
 121    ------------+---------+---------+---------+---------+---------+  180
        AGTACGTTACGTGGGCGACTATTGTTACTGTTTTGGCAGTTATTAAGACTATGGGGTTTC
                 S  C  N  A  P  A  D  N  N  D  K  T  V  N  N  S  D  T  P  K   -

        CTCATACTACCCAAAACACCACTTGAAACGCAGAACGTAGACAGGAGAAACTTGCTTCTG
 181    ------------+---------+---------+---------+---------+---------+  240
        GAGTATGATGGGTTTTGTGGTGAACTTTGCGTCTTGCATCTGTCCTCTTTGAACGAAGAC
                 L  I  L  P  K  T  P  L  E  T  Q  N  V  D  R  R  N  L  L  L   -

        GGACTCGGAGGTCTCTACGGCGCTGCCAACTTGACGACCATTCCGTCAGCCTTTGGCATT
 241    ------------+---------+---------+---------+---------+---------+  300
        CCTGAGCCTCCAGAGATGCCGCGACGGTTGAACTGCTGGTAAGGCAGTCGGAAACCGTAA
                 G  L  G  G  L  Y  G  A  A  N  L  T  T  I  P  S  A  F  G  I   -

        CCCATCGCTGCTCCAGACAATATTTCAGACTGTGTTGCTGCGACTTCAAACCTAAGGAAC
 301    ------------+---------+---------+---------+---------+---------+  360
        GGGTAGCGACGAGGTCTGTTATAAAGTCTGACACAACGACGCTGAAGTTTGGATTCCTTG
                 P  I  A  A  P  D  N  I  S  D  C  V  A  A  T  S  N  L  R  N   -

        AGCAAAGACGCTATAACGGGACTAGCGTGTTGTCCTCCGGTGCTTTCAACAAACAAACCA
 361    ------------+---------+---------+---------+---------+---------+  420
        TCGTTTCTGCGATATTCCCCTGATCGCACAACAGGAGGCCACGAAAGTTGTTTGTTTGGT
                 S  K  D  A  I  R  G  L  A  C  C  P  P  V  L  S  T  N  K  P   -

        ATGGATTACGTCCTTCCTTCAAACCCTGTGATTCGTGTTCGACCAGCTGCACAGAAAGCC
 421    ------------+---------+---------+---------+---------+---------+  480
        TACCTAATGCAGGAAGGAAGTTTGGGACACTAAGCACAAGCTGGTCGACGTGTCTTTCGG
                 M  D  Y  V  L  P  S  N  P  V  I  R  V  R  P  A  A  Q  K  A   -

        ACTGCCGATTACACTGCTAAGTATCAACAAGCAATTCAAGCCATGAAGGATCTCCCCGAG
 481    ------------+---------+---------+---------+---------+---------+  540
        TGACGGCTAATGTGACGATTCATAGTTGTTCGTTAAGTTCGGTACTTCCTAGAGGGGCTC
                 T  A  D  Y  T  A  K  Y  Q  Q  A  I  Q  A  M  K  D  L  P  E   -

        GACCACCCACATAGCTGGAAGCAACAAGGCAAGATTCACTGTGCTTATTGCAACGGTGGT
 541    ------------+---------+---------+---------+---------+---------+  600
        CTGGTGGGTGTATCGACCTTCGTTGTTCCGTTCTAAGTGACACGAATAACGTTGCCACCA
                 D  H  P  H  S  W  K  Q  Q  G  K  I  H  C  A  Y  C  N  G  G   -

        TACAATCAAGAACAAAGTGGTTACCCGAATTTACAACTTCAGATTCACAACTCATGGCTC
 601    ------------+---------+---------+---------+---------+---------+  660
        ATGTTAGTTCTTGTTTCACCAATGGGCTTAAATGTTGAAGTCTAAGTGTTGAGTACCGAG
                 Y  N  Q  E  Q  S  G  Y  P  N  L  Q  L  Q  I  H  N  S  W  L   -

        TTCTTTCCTTTCCACCGGTGGTACCTCTATTTCTACGAGAAGATATTGGGGAAGTTGATT
 651    ------------+---------+---------+---------+---------+---------+  720
        AAGAAAGGAAAGGTGGCCACCATGGAGATAAAGATGCTCTTCTATAACCCCTTCAACTAA
                 F  F  P  F  H  R  W  Y  L  Y  F  Y  E  K  I  L  G  K  L  I   -

        AATGATCCAACTTTCGCTCTACCTTACTGGAACTGGATAACCCTACTGGAATGGTTATT
 721    ------------+---------+---------+---------+---------+---------+  780
        TTACTAGGTTGAAAGCGAGATGGAATGACCTTGACCCTATTGGGATGACCTTACCAATAA
                 N  D  P  T  F  A  L  P  Y  W  N  W  D  N  P  T  G  M  V  I   -

        CCTCCCATGTTCGAACAGAACAGCAAACTAACTTCTGTTTGACCCTTTAAGGGATGCC
 731    ------------+---------+---------+---------+---------+---------+  840
        GGAGGGTACAAGCTTGTCTTGTCGTTTTGATTGAGAGACAAACTGGGAAATTCCCTACGC
                 P  A  M  F  E  Q  N  S  K  T  N  S  L  F  D  P  L  R  D  A   -
```

FIGURE 15-1

```
         AAACACCTCCCACCTTCTATCTTTGATGTTGAATATGCTGGTGCAGACACTGGTGCCACT
   841   ------------+---------+---------+---------+---------+---------+   900
         TTTGTGGAGGGTGGAAGATAGAAACTACAACTTATACGACCACGTCTGTGACCACGGTGA   -
          K  K  L  P  P  S  I  F  D  V  E  Y  A  G  A  D  T  G  A  T

         TGTATAGACCAGATAGCCATTAATCTGTCTTCAATGTACAGACAGATGGTCACCAACTCC
   901   ------------+---------+---------+---------+---------+---------+   960
         ACATATCTGGTCTATCGGTAATTAGACAGAAGTTACATGTCTGTCTACCAGTGGTTGAGG   -
          C  I  D  Q  I  A  I  N  L  S  S  M  Y  R  Q  M  V  T  N  S

         ACTGATACAAAACGATTCTTCGGTGGCGAATTTGTAGCTGGAAATGACCCTCTTGCGAGC
   961   ------------+---------+---------+---------+---------+---------+  1020
         TGACTATGTTTTGCTAAGAAGCCACCGCTTAAACATCGACCTTTACTGGGAGAACGCTCG   -
          T  D  T  K  R  F  F  G  G  E  F  V  A  G  N  D  P  L  A  S

         GAGTTCAACGTAGCTGGGACCGTAGAAGCTGGGGTTCACACTGCGGCTCACCGCTGGGTG
  1021   ------------+---------+---------+---------+---------+---------+  1080
         CTCAAGTTGCATCGACCCTGGCATCTTCGACCCCAAGTGTGACGCCGAGTGGCGACCCAC   -
          E  F  N  V  A  G  T  V  E  A  G  V  H  T  A  A  H  R  W  V

         GGTAATTCTAGGATGGCCAACAGCGAAGACATGGGGAACTTCTACTCCGCAGGATATGAT
  1081   ------------+---------+---------+---------+---------+---------+  1140
         CCATTAAGATCCTACCGGTTGTCGCTTCTGTACCCCTTGAAGATGAGGCGTCCTATACTA   -
          G  N  S  R  M  A  N  S  E  D  M  G  N  F  Y  S  A  G  Y  D

         CCTCTCTTTTACGTCCACCATGCGAATGTCGACAGGATGTGGCAAATCTGGAAAGATATT
  1141   ------------+---------+---------+---------+---------+---------+  1200
         GGAGAGAAAATGCAGGTGGTACGCTTACAGCTGTCCTACACCGTTTAGACCTTTCTATAA   -
          P  L  F  Y  V  H  H  A  N  V  D  R  M  W  Q  I  W  K  D  I

         GACAAGAAGACACACAAGGATCCGACCTCTGGCGACTGGCTAAATGCATCATACGTGTTT
  1201   ------------+---------+---------+---------+---------+---------+  1260
         CTGTTCTTCTGTGTGTTCCTAGGCTGGAGACCGCTGACCGATTTACGTAGTATGCACAAA   -
          D  K  K  T  H  K  D  P  T  S  G  D  W  L  N  A  S  Y  V  F

         TACGATGAGAATGAAAATCTTGTACGTGTCTACAACCGAGACTGTGTAGACATTAATCGG
  1261   ------------+---------+---------+---------+---------+---------+  1320
         ATGCTACTCTTACTTTTAGAACATGCACAGATGTTGGCTCTGACACATCTGTAATTAGCC   -
          Y  D  E  N  E  N  L  V  R  V  Y  N  R  D  C  V  D  I  N  R

         ATGGGATATGACTACGAAGGTCAGCAATCCCATGGATCCGTAGTCGGCCGACTGCACAT
  1321   ------------+---------+---------+---------+---------+---------+  1380
         TACCCTATACTGATGCTTTCCAGTCGTTAGGGTACCTAGGCATCAGCCGGCTGACGTGTA   -
          H  G  Y  D  Y  E  R  S  A  I  P  W  I  R  S  R  P  T  A  H

         GCGAAGGGGGCGAACGTTCCTGCTAAGTCTGCTGGAATCGTGCAGAAGGTGGAGGATATC
  1381   ------------+---------+---------+---------+---------+---------+  1440
         CGCTTCCCCCGCTTGCAACGACGATTCAGACGACCTTAGCACGTCTTCCACCTCCTATAG   -
          A  K  G  A  N  V  A  A  K  S  A  G  I  V  Q  K  V  E  D  I

         GTATTCCCGCTGAAGTTAAACAAGATAGTGAAGGTTCTAGTGAAGAGGCCAGCTACAAAC
  1441   ------------+---------+---------+---------+---------+---------+  1500
         CATAAGGGCGACTTCAATTTGTTCTATCACTTCCAAGATCACTTCTCCGGTCGATGTTTG   -
          V  F  P  L  K  L  N  K  I  V  K  V  L  V  K  R  P  A  T  N

         AGGACCAAGGAGGGAAAGGAGAAAGCAAATGAGCTGTTGTTCGTGAATGGAATCACGTTT
  1501   ------------+---------+---------+---------+---------+---------+  1560
         TCCTGGTTCCTCCCTTTCCTCTTTCGTTTACTCGACAACAAGCACTTACCTTAGTGCAAA   -
          R  T  K  E  G  K  E  K  A  N  E  L  L  F  V  N  G  I  T  F

         GATGCTGAGCCGGTTTCTAAAGATTGACGTGTTTGTCAACGACGTCGACGATGGAATTCAG
  1561   ------------+---------+---------+---------+---------+---------+  1620
         CTACGACTCGGCCAAAGATTTCTAACTGCACAAACAGTTGCTGCAGCTGCTACCTTAAGTC   -
          D  A  E  P  V  S  K  D  *
          D  A  E  R  F  L  K  I  D  V  F  V  N  D  V  D  D  G  I  Q

         ACCACCGCTGCTGATAGTGAGTTTCCTGGTAGTTTCGCACAGTTGCCCACATAACCATGCC
  1621   ------------+---------+---------+---------+---------+---------+  1680
         TGGTGGCGACGACTATCACTCAAACGACCATCAAAGCGTGTCAACGTGTATTGGTACCCG   -
          T  T  A  A  D  S  E  F  A  G  S  F  A  Q  L  P  H  N  H  G
```

FIGURE 15-2

```
      GACAAGATGTTTATGAGGAGTGGGGCAGCGTTCGGGATCACGGAGCTCTTGGAAGACATT
1681  ----------+---------+---------+---------+---------+---------+  1740
      CTGTTCTACAAATACTCCTCACCCCGTCGCAAGCCCTAGTGCCTCGAGAACCTTCTGTAA
       D  K  M  F  M  R  S  G  A  A  F  G  I  T  E  L  L  E  D  I   -

      GAAGCTGAAGGTGATGACTCTGTTGTTGTGACATTGGTGCCGAGAACAGGGTGTGATGAA
1741  ----------+---------+---------+---------+---------+---------+  1800
      CTTCGACTTCCACTACTGAGACAACAACACTGTAACCACGGCTCTTGTCCCACACTACTT
       E  A  E  G  D  D  S  V  V  V  T  L  V  P  R  T  G  C  D  E   -

      GTAACTATTGGCGAGATCAAGATTCAGCTGGTTCCCATTGTTTAAAGTCTATTGAAGTAA
1801  ----------+---------+---------+---------+---------+---------+  1860
      CATTGATAACCGCTCTAGTTCTAAGTCGACCAAGGGTAACAAATTTCAGATAACTTCATT
       V  T  I  G  E  I  K  I  Q  L  V  P  I  V  *

      TGCATTTTCAATTGTCATTAGTATGCATGGGTACGTAAATCTGTTCGCTGTCTGGTTATC
1861  ----------+---------+---------+---------+---------+---------+  1920
      ACGTAAAAGTTAACAGTAATCATACGTACCCATGCATTTAGACAAGCGACAGACCAATAG

      GAGGATTTTTGATGTTCTCGTAACCAAATAATAAGGATTGTCATTCCATGTTTGGAATCG
1921  ----------+---------+---------+---------+---------+---------+  1980
      CTCCTAAAAACTACAAGAGCATTGGTTTATTATTCCTAACAGTAAGGTACAAACCTTAGC

      TGTAACCGCAGGCATGCATATGTTTGATTGTTATTTTTACTTGAAGCACTTCTGTTTTAG
1981  ----------+---------+---------+---------+---------+---------+  2040
      ACATTGGCGTCCGTACGTATACAAACTAACAATAAAAATGAACTTCGTGAAGACAAAATC

      TAAAAAAAAAAAAAAAAA
2041  ------------+------  2057
      ATTTTTTTTTTTTTTTTT
```

FIGURE 15-3